

sequence listing
SEQUENCE LISTING

<110> Kock, Michael
Frank, Markus
Badur, Ralf

<120> Novel Selection Processes

<130> 532622010400

<140> To be assigned

<141> 2005-01-24

<160> 71

<170> PatentIn Ver. 2.1

<210> 1

<211> 1284

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1281)

<223> coding for cytosine deaminase (codA)

<400> 1

gtg tcg aat aac gct tta caa aca att att aac gcc cgg tta cca ggc	48
Val Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly	
1 5 10 15	
gaa gag ggg ctg tgg cag att cat ctg cag gac gga aaa atc agc gcc	96
Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala	
20 25 30	
att gat gcg caa tcc ggc gtg atg ccc ata act gaa aac agc ctg gat	144
Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp	
35 40 45	
gcc gaa caa ggt tta gtt ata ccg ccg ttt gtg gag cca cat att cac	192
Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His	
50 55 60	
ctg gac acc acg caa acc gcc gga caa ccg aac tgg aat cag tcc ggc	240
Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly	
65 70 75 80	
acg ctg ttt gaa ggc att gaa cgc tgg gcc gag cgc aaa gcg tta tta	288
Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu	
85 90 95	
acc cat gac gat gtg aaa caa cgc gca tgg caa acg ctg aaa tgg cag	336
Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln	
100 105 110	
att gcc aac ggc att cag cat gtg cgt acc cat gtc gat gtt tcg gat	384
Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp	
115 120 125	
gca acg cta act gcg ctg aaa gca atg ctg gaa gtg aag cag gaa gtc	432
Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val	
130 135 140	

sequence listing																
gcg	ccg	tgg	att	gat	ctg	caa	atc	gtc	gcc	ttc	cct	cag	gaa	ggg	att	480
Ala	Pro	Trp	Ile	Asp	Leu	Gln	Ile	Val	Ala	Phe	Pro	Gln	Glu	Gly	Ile	
145					150					155					160	
ttg	tcg	tat	ccc	aac	ggt	gaa	gcg	ttg	ctg	gaa	gag	gcg	tta	cgc	tta	528
Leu	Ser	Tyr	Pro	Asn	Gly	Glu	Ala	Leu	Leu	Glu	Glu	Ala	Leu	Arg	Leu	
				165				170						175		
ggg	gca	gat	gta	gtg	ggg	gcg	att	ccg	cat	ttt	gaa	ttt	acc	cgt	gaa	576
Gly	Ala	Asp	Val	Val	Gly	Ala	Ile	Pro	His	Phe	Glu	Phe	Thr	Arg	Glu	
			180					185					190			
tac	ggc	gtg	gag	tcg	ctg	cat	aaa	acc	ttc	gcc	ctg	gcg	caa	aaa	tac	624
Tyr	Gly	Val	Glu	Ser	Leu	His	Lys	Thr	Phe	Ala	Leu	Ala	Gln	Lys	Tyr	
		195					200					205				
gac	cgt	ctc	atc	gac	gtt	cac	tgt	gat	gag	atc	gat	gac	gag	cag	tcg	672
Asp	Arg	Leu	Ile	Asp	Val	His	Cys	Asp	Glu	Ile	Asp	Asp	Glu	Gln	Ser	
	210					215					220					
cgc	ttt	gtc	gaa	acc	gtt	gct	gcc	ctg	gcg	cac	cat	gaa	ggc	atg	ggc	720
Arg	Phe	Val	Glu	Thr	Val	Ala	Ala	Leu	Ala	His	His	Glu	Gly	Met	Gly	
225					230					235					240	
gcg	cga	gtc	acc	gcc	agc	cac	acc	acg	gca	atg	cac	tcc	tat	aac	ggg	768
Ala	Arg	Val	Thr	Ala	Ser	His	Thr	Thr	Ala	Met	His	Ser	Tyr	Asn	Gly	
				245					250					255		
gcg	tat	acc	tca	cgc	ctg	ttc	cgc	ttg	ctg	aaa	atg	tcc	ggt	att	aac	816
Ala	Tyr	Thr	Ser	Arg	Leu	Phe	Arg	Leu	Leu	Lys	Met	Ser	Gly	Ile	Asn	
			260					265					270			
ttt	gtc	gcc	aac	ccg	ctg	gtc	aat	att	cat	ctg	caa	gga	cgt	ttc	gat	864
Phe	Val	Ala	Asn	Pro	Leu	Val	Asn	Ile	His	Leu	Gln	Gly	Arg	Phe	Asp	
		275					280					285				
acg	tat	cca	aaa	cgt	cgc	ggc	atc	acg	cgc	gtt	aaa	gag	atg	ctg	gag	912
Thr	Tyr	Pro	Lys	Arg	Arg	Gly	Ile	Thr	Arg	Val	Lys	Glu	Met	Leu	Glu	
	290					295					300					
tcc	ggc	att	aac	gtc	tgc	ttt	ggt	cac	gat	gat	gtc	ttc	gat	ccg	tgg	960
Ser	Gly	Ile	Asn	Val	Cys	Phe	Gly	His	Asp	Asp	Val	Phe	Asp	Pro	Trp	
305					310					315					320	
tat	ccg	ctg	gga	acg	gcg	aat	atg	ctg	caa	gtg	ctg	cat	atg	ggg	ctg	1008
Tyr	Pro	Leu	Gly	Thr	Ala	Asn	Met	Leu	Gln	Val	Leu	His	Met	Gly	Leu	
				325					330					335		
cat	gtt	tgc	cag	ttg	atg	ggc	tac	ggg	cag	att	aac	gat	ggc	ctg	aat	1056
His	Val	Cys	Gln	Leu	Met	Gly	Tyr	Gly	Gln	Ile	Asn	Asp	Gly	Leu	Asn	
			340					345					350			
tta	atc	acc	cac	cac	agc	gca	agg	acg	ttg	aat	ttg	cag	gat	tac	ggc	1104
Leu	Ile	Thr	His	His	Ser	Ala	Arg	Thr	Leu	Asn	Leu	Gln	Asp	Tyr	Gly	
		355					360					365				
att	gcc	gcc	gga	aac	agc	gcc	aac	ctg	att	atc	ctg	ccg	gct	gaa	aat	1152
Ile	Ala	Ala	Gly	Asn	Ser	Ala	Asn	Leu	Ile	Ile	Leu	Pro	Ala	Glu	Asn	
	370					375					380					
ggg	ttt	gat	gcg	ctg	cgc	cgt	cag	gtt	ccg	gta	cgt	tat	tcg	gta	cgt	1200
Gly	Phe	Asp	Ala	Leu	Arg	Arg	Gln	Val	Pro	Val	Arg	Tyr	Ser	Val	Arg	
385					390					395					400	

sequence listing

ggc ggc aag gtg att gcc agc aca caa ccg gca caa acc acc gta tat 1248
Gly Gly Lys Val Ile Ala Ser Thr Gln Pro Ala Gln Thr Thr Val Tyr
405 410 415

ctg gag cag cca gaa gcc atc gat tac aaa cgt tga 1284
Leu Glu Gln Pro Glu Ala Ile Asp Tyr Lys Arg
420 425

<210> 2
<211> 427
<212> PRT
<213> Escherichia coli

<400> 2
Val Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly
1 5 10 15
Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala
20 25 30
Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp
35 40 45
Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His
50 55 60
Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly
65 70 75 80
Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu
85 90 95
Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln
100 105 110
Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp
115 120 125
Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val
130 135 140
Ala Pro Trp Ile Asp Leu Gln Ile Val Ala Phe Pro Gln Glu Gly Ile
145 150 155 160
Leu Ser Tyr Pro Asn Gly Glu Ala Leu Leu Glu Glu Ala Leu Arg Leu
165 170 175
Gly Ala Asp Val Val Gly Ala Ile Pro His Phe Glu Phe Thr Arg Glu
180 185 190
Tyr Gly Val Glu Ser Leu His Lys Thr Phe Ala Leu Ala Gln Lys Tyr
195 200 205
Asp Arg Leu Ile Asp Val His Cys Asp Glu Ile Asp Asp Glu Gln Ser
210 215 220
Arg Phe Val Glu Thr Val Ala Ala Leu Ala His His Glu Gly Met Gly
225 230 235 240
Ala Arg Val Thr Ala Ser His Thr Thr Ala Met His Ser Tyr Asn Gly
245 250 255

sequence listing

Ala Tyr Thr Ser Arg Leu Phe Arg Leu Leu Lys Met Ser Gly Ile Asn
260 265 270
Phe Val Ala Asn Pro Leu Val Asn Ile His Leu Gln Gly Arg Phe Asp
275 280 285
Thr Tyr Pro Lys Arg Arg Gly Ile Thr Arg Val Lys Glu Met Leu Glu
290 295 300
Ser Gly Ile Asn Val Cys Phe Gly His Asp Asp Val Phe Asp Pro Trp
305 310 315 320
Tyr Pro Leu Gly Thr Ala Asn Met Leu Gln Val Leu His Met Gly Leu
325 330 335
His Val Cys Gln Leu Met Gly Tyr Gly Gln Ile Asn Asp Gly Leu Asn
340 345 350
Leu Ile Thr His His Ser Ala Arg Thr Leu Asn Leu Gln Asp Tyr Gly
355 360 365
Ile Ala Ala Gly Asn Ser Ala Asn Leu Ile Ile Leu Pro Ala Glu Asn
370 375 380
Gly Phe Asp Ala Leu Arg Arg Gln Val Pro Val Arg Tyr Ser Val Arg
385 390 395 400
Gly Gly Lys Val Ile Ala Ser Thr Gln Pro Ala Gln Thr Thr Val Tyr
405 410 415
Leu Glu Gln Pro Glu Ala Ile Asp Tyr Lys Arg
420 425

<210> 3

<211> 1284

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
cytosine deaminase (codA)

<220>

<221> misc_feature

<222> (1)..(3)

<223> mutation of GTG to ATG start codon for expression
in eukaryotic hosts

<220>

<221> CDS

<222> (1)..(1281)

<223> coding for cytosine deaminase (codA)

<400> 3

atg tcg aat aac gct tta caa aca att att aac gcc cgg tta cca ggc 48
Met Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly
1 5 10 15

gaa gag ggg ctg tgg cag att cat ctg cag gac gga aaa atc agc gcc 96
Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala
20 25 30

att gat gcg caa tcc ggc gtg atg ccc ata act gaa aac agc ctg gat 144
Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp
35 40 45

sequence listing

gcc gaa caa ggt tta gtt ata ccg ccg ttt gtg gag cca cat att cac	192
Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His	
50 55 60	
ctg gac acc acg caa acc gcc gga caa ccg aac tgg aat cag tcc ggc	240
Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly	
65 70 75 80	
acg ctg ttt gaa ggc att gaa cgc tgg gcc gag cgc aaa gcg tta tta	288
Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu	
85 90 95	
acc cat gac gat gtg aaa caa cgc gca tgg caa acg ctg aaa tgg cag	336
Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln	
100 105 110	
att gcc aac ggc att cag cat gtg cgt acc cat gtc gat gtt tcg gat	384
Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp	
115 120 125	
gca acg cta act gcg ctg aaa gca atg ctg gaa gtg aag cag gaa gtc	432
Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val	
130 135 140	
gcg ccg tgg att gat ctg caa atc gtc gcc ttc cct cag gaa ggg att	480
Ala Pro Trp Ile Asp Leu Gln Ile Val Ala Phe Pro Gln Glu Gly Ile	
145 150 155 160	
ttg tcg tat ccc aac ggt gaa gcg ttg ctg gaa gag gcg tta cgc tta	528
Leu Ser Tyr Pro Asn Gly Glu Ala Leu Leu Glu Glu Ala Leu Arg Leu	
165 170 175	
ggg gca gat gta gtg ggg gcg att ccg cat ttt gaa ttt acc cgt gaa	576
Gly Ala Asp Val Val Gly Ala Ile Pro His Phe Glu Phe Thr Arg Glu	
180 185 190	
tac ggc gtg gag tcg ctg cat aaa acc ttc gcc ctg gcg caa aaa tac	624
Tyr Gly Val Glu Ser Leu His Lys Thr Phe Ala Leu Ala Gln Lys Tyr	
195 200 205	
gac cgt ctc atc gac gtt cac tgt gat gag atc gat gac gag cag tcg	672
Asp Arg Leu Ile Asp Val His Cys Asp Glu Ile Asp Asp Glu Gln Ser	
210 215 220	
cgc ttt gtc gaa acc gtt gct gcc ctg gcg cac cat gaa ggc atg ggc	720
Arg Phe Val Glu Thr Val Ala Ala Leu Ala His His Glu Gly Met Gly	
225 230 235 240	
gcg cga gtc acc gcc agc cac acc acg gca atg cac tcc tat aac ggg	768
Ala Arg Val Thr Ala Ser His Thr Thr Ala Met His Ser Tyr Asn Gly	
245 250 255	
gcg tat acc tca cgc ctg ttc cgc ttg ctg aaa atg tcc ggt att aac	816
Ala Tyr Thr Ser Arg Leu Phe Arg Leu Leu Lys Met Ser Gly Ile Asn	
260 265 270	
ttt gtc gcc aac ccg ctg gtc aat att cat ctg caa gga cgt ttc gat	864
Phe Val Ala Asn Pro Leu Val Asn Ile His Leu Gln Gly Arg Phe Asp	
275 280 285	
acg tat cca aaa cgt cgc ggc atc acg cgc gtt aaa gag atg ctg gag	912
Thr Tyr Pro Lys Arg Arg Gly Ile Thr Arg Val Lys Glu Met Leu Glu	

sequence listing
300

290	295		
tcc ggc att aac gtc tgc ttt ggt cac gat gat gtc ttc gat ccg tgg			960
Ser Gly Ile Asn Val Cys Phe Gly His Asp Asp Val Phe Asp Pro Trp			
305	310	315	320
tat ccg ctg gga acg gcg aat atg ctg caa gtg ctg cat atg ggg ctg			1008
Tyr Pro Leu Gly Thr Ala Asn Met Leu Gln Val Leu His Met Gly Leu			
	325	330	335
cat gtt tgc cag ttg atg ggc tac ggg cag att aac gat ggc ctg aat			1056
His Val Cys Gln Leu Met Gly Tyr Gly Gln Ile Asn Asp Gly Leu Asn			
	340	345	350
tta atc acc cac cac agc gca agg acg ttg aat ttg cag gat tac ggc			1104
Leu Ile Thr His His Ser Ala Arg Thr Leu Asn Leu Gln Asp Tyr Gly			
	355	360	365
att gcc gcc gga aac agc gcc aac ctg att atc ctg ccg gct gaa aat			1152
Ile Ala Ala Gly Asn Ser Ala Asn Leu Ile Ile Leu Pro Ala Glu Asn			
	370	375	380
ggg ttt gat gcg ctg cgc cgt cag gtt ccg gta cgt tat tcg gta cgt			1200
Gly Phe Asp Ala Leu Arg Arg Gln Val Pro Val Arg Tyr Ser Val Arg			
	385	390	400
ggc ggc aag gtg att gcc agc aca caa ccg gca caa acc acc gta tat			1248
Gly Gly Lys Val Ile Ala Ser Thr Gln Pro Ala Gln Thr Thr Val Tyr			
	405	410	415
ctg gag cag cca gaa gcc atc gat tac aaa cgt tga			1284
Leu Glu Gln Pro Glu Ala Ile Asp Tyr Lys Arg			
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<210> 4

<211> 427

<212> PRT

<213> Artificial sequence

<223> Description of the artificial sequence: coding for
cytosine deaminase (codA)

<400> 4

Met Ser Asn Asn Ala Leu Gln Thr Ile Ile Asn Ala Arg Leu Pro Gly	
1 5 10 15	
Glu Glu Gly Leu Trp Gln Ile His Leu Gln Asp Gly Lys Ile Ser Ala	
20 25 30	
Ile Asp Ala Gln Ser Gly Val Met Pro Ile Thr Glu Asn Ser Leu Asp	
35 40 45	
Ala Glu Gln Gly Leu Val Ile Pro Pro Phe Val Glu Pro His Ile His	
50 55 60	
Leu Asp Thr Thr Gln Thr Ala Gly Gln Pro Asn Trp Asn Gln Ser Gly	
65 70 75 80	
Thr Leu Phe Glu Gly Ile Glu Arg Trp Ala Glu Arg Lys Ala Leu Leu	
85 90 95	
Thr His Asp Asp Val Lys Gln Arg Ala Trp Gln Thr Leu Lys Trp Gln	
100 105 110	

sequence listing

Ile Ala Asn Gly Ile Gln His Val Arg Thr His Val Asp Val Ser Asp
115 120 125

Ala Thr Leu Thr Ala Leu Lys Ala Met Leu Glu Val Lys Gln Glu Val
130 135 140

Ala Pro Trp Ile Asp Leu Gln Ile Val Ala Phe Pro Gln Glu Gly Ile
145 150 155 160

Leu Ser Tyr Pro Asn Gly Glu Ala Leu Leu Glu Glu Ala Leu Arg Leu
165 170 175

Gly Ala Asp Val Val Gly Ala Ile Pro His Phe Glu Phe Thr Arg Glu
180 185 190

Tyr Gly Val Glu Ser Leu His Lys Thr Phe Ala Leu Ala Gln Lys Tyr
195 200 205

Asp Arg Leu Ile Asp Val His Cys Asp Glu Ile Asp Asp Glu Gln Ser
210 215 220

Arg Phe Val Glu Thr Val Ala Ala Leu Ala His His Glu Gly Met Gly
225 230 235 240

Ala Arg Val Thr Ala Ser His Thr Thr Ala Met His Ser Tyr Asn Gly
245 250 255

Ala Tyr Thr Ser Arg Leu Phe Arg Leu Leu Lys Met Ser Gly Ile Asn
260 265 270

Phe Val Ala Asn Pro Leu Val Asn Ile His Leu Gln Gly Arg Phe Asp
275 280 285

Thr Tyr Pro Lys Arg Arg Gly Ile Thr Arg Val Lys Glu Met Leu Glu
290 295 300

Ser Gly Ile Asn Val Cys Phe Gly His Asp Asp Val Phe Asp Pro Trp
305 310 315 320

Tyr Pro Leu Gly Thr Ala Asn Met Leu Gln Val Leu His Met Gly Leu
325 330 335

His Val Cys Gln Leu Met Gly Tyr Gly Gln Ile Asn Asp Gly Leu Asn
340 345 350

Leu Ile Thr His His Ser Ala Arg Thr Leu Asn Leu Gln Asp Tyr Gly
355 360 365

Ile Ala Ala Gly Asn Ser Ala Asn Leu Ile Ile Leu Pro Ala Glu Asn
370 375 380

Gly Phe Asp Ala Leu Arg Arg Gln Val Pro Val Arg Tyr Ser Val Arg
385 390 395 400

Gly Gly Lys Val Ile Ala Ser Thr Gln Pro Ala Gln Thr Thr Val Tyr
405 410 415

Leu Glu Gln Pro Glu Ala Ile Asp Tyr Lys Arg
420 425

<210> 5
<211> 1221
<212> DNA

sequence listing

<213> Streptomyces griseolus

<220>

<221> CDS

<222> (1)..(1218)

<223> coding for cytochrome P450-Su1 (suac)

<400> 5

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1 5 10 15	
ccg agc aac cgg agc tgt ccc tac cag tta ccg gac ggc tac gcc cag	96
Pro Ser Asn Arg Ser Cys Pro Tyr Gln Leu Pro Asp Gly Tyr Ala Gln	
20 25 30	
ctc cgg gac acc ccc ggc ccc ctg cac cgg gtg acg ctc tac gac ggc	144
Leu Arg Asp Thr Pro Gly Pro Leu His Arg Val Thr Leu Tyr Asp Gly	
35 40 45	
cgt cag gcg tgg gtg gtg acc aag cac gag gcc gcg cgc aaa ctg ctc	192
Arg Gln Ala Trp Val Val Thr Lys His Glu Ala Ala Arg Lys Leu Leu	
50 55 60	
ggc gac ccc cgg ctg tcc tcc aac cgg acg gac gac aac ttc ccc gcc	240
Gly Asp Pro Arg Leu Ser Ser Asn Arg Thr Asp Asp Asn Phe Pro Ala	
65 70 75 80	
acg tca ccg cgc ttc gag gcc gtc cgg gag agc ccg cag gcg ttc atc	288
Thr Ser Pro Arg Phe Glu Ala Val Arg Glu Ser Pro Gln Ala Phe Ile	
85 90 95	
ggc ctg gac ccg ccc gag cac ggc acc cgg cgg cgg atg acg atc agc	336
Gly Leu Asp Pro Pro Glu His Gly Thr Arg Arg Arg Met Thr Ile Ser	
100 105 110	
gag ttc acc gtc aag cgg atc aag ggc atg cgc ccc gag gtc gag gag	384
Glu Phe Thr Val Lys Arg Ile Lys Gly Met Arg Pro Glu Val Glu Glu	
115 120 125	
gtg gtg cac ggc ttc ctc gac gag atg ctg gcc gcc ggc ccg acc gcc	432
Val Val His Gly Phe Leu Asp Glu Met Leu Ala Ala Gly Pro Thr Ala	
130 135 140	
gac ctg gtc agt cag ttc gcg ctg ccg gtg ccc tcc atg gtg atc tgc	480
Asp Leu Val Ser Gln Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys	
145 150 155 160	
cga ctc ctc ggc gtg ccc tac gcc gac cac gag ttc ttc cag gac gcg	528
Arg Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe Gln Asp Ala	
165 170 175	
agc aag cgg ctg gtg cag tcc acg gac gcg cag agc gcg ctc acc gcg	576
Ser Lys Arg Leu Val Gln Ser Thr Asp Ala Gln Ser Ala Leu Thr Ala	
180 185 190	
cgg aac gac ctc gcg ggt tac ctg gac ggc ctc atc acc cag ttc cag	624
Arg Asn Asp Leu Ala Gly Tyr Leu Asp Gly Leu Ile Thr Gln Phe Gln	
195 200 205	
acc gaa ccg ggc gcg ggc ctg gtg ggc gct ctg gtc gcc gac cag ctg	672
Thr Glu Pro Gly Ala Gly Leu Val Gly Ala Leu Val Ala Asp Gln Leu	
210 215 220	

sequence listing

gcc aac ggc gag atc gac cgt gag gaa ctg atc tcc acc gcg atg ctg	720
Ala Asn Gly Glu Ile Asp Arg Glu Glu Leu Ile Ser Thr Ala Met Leu	
225 230 235 240	
ctc ctc atc gcc ggc cac gag acc acg gcc tcg atg acc tcc ctc agc	768
Leu Leu Ile Ala Gly His Glu Thr Thr Ala Ser Met Thr Ser Leu Ser	
245 250 255	
gtg atc acc ctg ctg gac cac ccc gag cag tac gcc gcc ctg cgc gcc	816
Val Ile Thr Leu Leu Asp His Pro Glu Gln Tyr Ala Ala Leu Arg Ala	
260 265 270	
gac cgc agc ctc gtg ccc ggc gcg gtg gag gaa ctg ctc cgc tac ctc	864
Asp Arg Ser Leu Val Pro Gly Ala Val Glu Glu Leu Leu Arg Tyr Leu	
275 280 285	
gcc atc gcc gac atc gcg ggc ggc cgc gtc gcc acg gcg gac atc gag	912
Ala Ile Ala Asp Ile Ala Gly Gly Arg Val Ala Thr Ala Asp Ile Glu	
290 295 300	
gtc gag ggg cac ctc atc cgg gcc ggc gag ggc gtg atc gtc gtc aac	960
Val Glu Gly His Leu Ile Arg Ala Gly Glu Gly Val Ile Val Val Asn	
305 310 315 320	
tcg ata gcc aac cgg gac ggc acg gtg tac gag gac ccg gac gcc ctc	1008
Ser Ile Ala Asn Arg Asp Gly Thr Val Tyr Glu Asp Pro Asp Ala Leu	
325 330 335	
gac atc cac cgc tcc gcg cgc cac cac ctc gcc ttc ggc ttc ggc gtg	1056
Asp Ile His Arg Ser Ala Arg His His Leu Ala Phe Gly Phe Gly Val	
340 345 350	
cac cag tgc ctg ggc cag aac ctc gcc cgg ctg gag ctg gag gtc atc	1104
His Gln Cys Leu Gly Gln Asn Leu Ala Arg Leu Glu Leu Glu Val Ile	
355 360 365	
ctc aac gcc ctc atg gac cgc gtc ccg acg ctg cga ctg gcc gtc ccc	1152
Leu Asn Ala Leu Met Asp Arg Val Pro Thr Leu Arg Leu Ala Val Pro	
370 375 380	
gtc gag cag ttg gtg ctg cgg ccg ggt acg acg atc cag ggc gtc aac	1200
Val Glu Gln Leu Val Leu Arg Pro Gly Thr Thr Ile Gln Gly Val Asn	
385 390 395 400	
gaa ctc ccg gtc acc tgg tga	1221
Glu Leu Pro Val Thr Trp	
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<210> 6

<211> 406

<212> PRT

<213> Streptomyces griseolus

<400> 6

Met Thr Asp Thr Ala Thr Thr Pro Gln Thr Thr Asp Ala Pro Ala Phe

1

5

10

15

Pro Ser Asn Arg Ser Cys Pro Tyr Gln Leu Pro Asp Gly Tyr Ala Gln

20

25

30

Leu Arg Asp Thr Pro Gly Pro Leu His Arg Val Thr Leu Tyr Asp Gly

35

40

45

sequence listing

Arg Gln Ala Trp Val Val Thr Lys His Glu Ala Ala Arg Lys Leu Leu
50 55 60

Gly Asp Pro Arg Leu Ser Ser Asn Arg Thr Asp Asp Asn Phe Pro Ala
65 70 75 80

Thr Ser Pro Arg Phe Glu Ala Val Arg Glu Ser Pro Gln Ala Phe Ile
85 90 95

Gly Leu Asp Pro Pro Glu His Gly Thr Arg Arg Arg Met Thr Ile Ser
100 105 110

Glu Phe Thr Val Lys Arg Ile Lys Gly Met Arg Pro Glu Val Glu Glu
115 120 125

Val Val His Gly Phe Leu Asp Glu Met Leu Ala Ala Gly Pro Thr Ala
130 135 140

Asp Leu Val Ser Gln Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys
145 150 155 160

Arg Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe Gln Asp Ala
165 170 175

Ser Lys Arg Leu Val Gln Ser Thr Asp Ala Gln Ser Ala Leu Thr Ala
180 185 190

Arg Asn Asp Leu Ala Gly Tyr Leu Asp Gly Leu Ile Thr Gln Phe Gln
195 200 205

Thr Glu Pro Gly Ala Gly Leu Val Gly Ala Leu Val Ala Asp Gln Leu
210 215 220

Ala Asn Gly Glu Ile Asp Arg Glu Glu Leu Ile Ser Thr Ala Met Leu
225 230 235 240

Leu Leu Ile Ala Gly His Glu Thr Thr Ala Ser Met Thr Ser Leu Ser
245 250 255

Val Ile Thr Leu Leu Asp His Pro Glu Gln Tyr Ala Ala Leu Arg Ala
260 265 270

Asp Arg Ser Leu Val Pro Gly Ala Val Glu Glu Leu Leu Arg Tyr Leu
275 280 285

Ala Ile Ala Asp Ile Ala Gly Gly Arg Val Ala Thr Ala Asp Ile Glu
290 295 300

Val Glu Gly His Leu Ile Arg Ala Gly Glu Gly Val Ile Val Val Asn
305 310 315 320

Ser Ile Ala Asn Arg Asp Gly Thr Val Tyr Glu Asp Pro Asp Ala Leu
325 330 335

Asp Ile His Arg Ser Ala Arg His His Leu Ala Phe Gly Phe Gly Val
340 345 350

His Gln Cys Leu Gly Gln Asn Leu Ala Arg Leu Glu Leu Glu Val Ile
355 360 365

Leu Asn Ala Leu Met Asp Arg Val Pro Thr Leu Arg Leu Ala Val Pro
370 375 380

sequence listing

Val Glu Gln Leu Val Leu Arg Pro Gly Thr Thr Ile Gln Gly Val Asn
385 390 395 400

Glu Leu Pro Val Thr Trp
405

<210> 7

<211> 1404

<212> DNA

<213> Agrobacterium tumefaciens

<220>

<221> CDS

<222> (1)..(1401)

<223> coding for indoleacetamide hydrolase (tms2)

<400> 7

atg gtg ccc att acc tcg tta gca caa acc cta gaa cgc ctg aga cgg 48
Met Val Pro Ile Thr Ser Leu Ala Gln Thr Leu Glu Arg Leu Arg Arg
1 5 10 15

aaa gac tac tcc tgc tta gaa cta gta gaa act ctg ata gcg cgt tgc 96
Lys Asp Tyr Ser Cys Leu Glu Leu Val Glu Thr Leu Ile Ala Arg Cys
20 25 30

caa gct gca aaa cca tta aat gcc ctt ctg gct aca gac tgg gat ggc 144
Gln Ala Ala Lys Pro Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Gly
35 40 45

ttg cgg cga agc gcc aaa aaa att gat cgt cat gga aac gcc gga tta 192
Leu Arg Arg Ser Ala Lys Lys Ile Asp Arg His Gly Asn Ala Gly Leu
50 55 60

ggt ctt tgc ggc att cca ctc tgt ttt aag gcg aac atc gcg acc ggc 240
Gly Leu Cys Gly Ile Pro Leu Cys Phe Lys Ala Asn Ile Ala Thr Gly
65 70 75 80

ata ttt cct aca agc gct gct act ccg gcg ctg ata aac cac ttg cca 288
Ile Phe Pro Thr Ser Ala Ala Thr Pro Ala Leu Ile Asn His Leu Pro
85 90 95

aag ata cca tcc cgc gtc gca gaa aga ctt ttt tca gct gga gca ctg 336
Lys Ile Pro Ser Arg Val Ala Glu Arg Leu Phe Ser Ala Gly Ala Leu
100 105 110

ccg ggt gcc tcg gga aac atg cat gag tta tcg ttt gga att acg agc 384
Pro Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser
115 120 125

aac aac tat gcc acc ggt gcg gtg cgg aac ccg tgg aat cca agt ctg 432
Asn Asn Tyr Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu
130 135 140

ata cca gga ggc tca agc ggt gtg gct gct gcg gtg gca agc cga 480
Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Val Ala Ser Arg
145 150 155 160

ttg atg tta ggc ggc ata ggc acc gat acc ggt gca tct gtt cgc cta 528
Leu Met Leu Gly Gly Ile Gly Thr Asp Thr Gly Ala Ser Val Arg Leu
165 170 175

ccc gca gcc ctg tgt ggc gta gta gga ttt cga ccg acg ctt gct cga 576
Pro Ala Ala Leu Cys Gly Val Val Gly Phe Arg Pro Thr Leu Ala Arg
180 185 190

tat cca aga gat cgg ata ata ccg gtc agc ccc acc cgg gac acc gcc 624

sequence listing															
Tyr	Pro	Arg	Asp	Arg	Ile	Ile	Pro	Val	Ser	Pro	Thr	Arg	Asp	Thr	Ala
		195					200					205			
gga	atc	ata	gcg	cag	tgc	gta	gcc	gat	gtt	ata	atc	ctc	gac	cag	gtg
Gly	Ile	Ile	Ala	Gln	Cys	Val	Ala	Asp	Val	Ile	Ile	Leu	Asp	Gln	Val
	210					215					220				672
att	tcc	gga	cgg	tcg	gcg	aaa	att	tca	ccc	atg	ccg	ctg	aag	ggg	ctt
Ile	Ser	Gly	Arg	Ser	Ala	Lys	Ile	Ser	Pro	Met	Pro	Leu	Lys	Gly	Leu
225					230					235					720
cgg	atc	ggc	ctc	ccc	act	acc	tac	ttt	tac	gat	gac	ctt	gat	gct	gat
Arg	Ile	Gly	Leu	Pro	Thr	Thr	Tyr	Phe	Tyr	Asp	Asp	Leu	Asp	Ala	Asp
				245					250					255	768
gtg	gcc	ttc	gca	gct	gaa	acg	acg	att	cgc	ttg	cta	gcc	aac	aga	ggc
Val	Ala	Phe	Ala	Ala	Glu	Thr	Thr	Ile	Arg	Leu	Leu	Ala	Asn	Arg	Gly
			260					265					270		816
gta	acc	ttt	gtt	gaa	gcc	gac	atc	ccc	cac	cta	gag	gaa	ctg	aat	agt
Val	Thr	Phe	Val	Glu	Ala	Asp	Ile	Pro	His	Leu	Glu	Glu	Leu	Asn	Ser
		275					280					285			864
ggg	gca	agt	ttg	cca	att	gcg	ctt	tac	gaa	ttt	cca	cac	gct	cta	aaa
Gly	Ala	Ser	Leu	Pro	Ile	Ala	Leu	Tyr	Glu	Phe	Pro	His	Ala	Leu	Lys
	290					295					300				912
aag	tat	ctc	gac	gat	ttt	gtg	gga	aca	gtt	tct	ttt	tct	gac	gtt	atc
Lys	Tyr	Leu	Asp	Asp	Phe	Val	Gly	Thr	Val	Ser	Phe	Ser	Asp	Val	Ile
305					310					315					960
aaa	gga	att	cgt	agc	ccc	gat	gta	gcg	aac	att	gtc	agt	gcg	caa	att
Lys	Gly	Ile	Arg	Ser	Pro	Asp	Val	Ala	Asn	Ile	Val	Ser	Ala	Gln	Ile
				325					330					335	1008
gat	ggg	cat	caa	att	tcc	aac	gat	gaa	tat	gaa	ctg	gcg	cgt	caa	tcc
Asp	Gly	His	Gln	Ile	Ser	Asn	Asp	Glu	Tyr	Glu	Leu	Ala	Arg	Gln	Ser
			340					345					350		1056
ttc	agg	cca	agg	ctc	cag	gcc	act	tat	cgg	aat	tac	ttc	aga	ctc	tat
Phe	Arg	Pro	Arg	Leu	Gln	Ala	Thr	Tyr	Arg	Asn	Tyr	Phe	Arg	Leu	Tyr
		355					360					365			1104
cag	tta	gat	gca	atc	ctt	ttc	cca	act	gca	ccc	tta	gcg	gcc	aaa	gcc
Gln	Leu	Asp	Ala	Ile	Leu	Phe	Pro	Thr	Ala	Pro	Leu	Ala	Ala	Lys	Ala
	370					375					380				1152
ata	ggt	cag	gag	tcg	tca	gtc	atc	cac	aat	ggc	tca	atg	atg	aac	act
Ile	Gly	Gln	Glu	Ser	Ser	Val	Ile	His	Asn	Gly	Ser	Met	Met	Asn	Thr
385					390					395					1200
ttc	aag	atc	tac	gtg	cga	aat	gtg	gac	cca	agc	agc	aac	gca	ggc	cta
Phe	Lys	Ile	Tyr	Val	Arg	Asn	Val	Asp	Pro	Ser	Ser	Asn	Ala	Gly	Leu
				405					410					415	1248
cct	ggg	ttg	agc	ctt	cct	gcc	tgc	ctt	aca	cct	gat	cgc	ttg	cct	gtt
Pro	Gly	Leu	Ser	Leu	Pro	Ala	Cys	Leu	Thr	Pro	Asp	Arg	Leu	Pro	Val
			420					425					430		1296
gga	atg	gaa	att	gat	gga	tta	gcg	ggg	tca	gac	cac	cgt	ctg	tta	gca
Gly	Met	Glu	Ile	Asp	Gly	Leu	Ala	Gly	Ser	Asp	His	Arg	Leu	Leu	Ala
		435					440					445			1344

sequence listing

atc	ggg	gca	gca	tta	gaa	aaa	gcc	ata	aat	ttt	cct	tcc	ttt	ccc	gat	1392
Ile	Gly	Ala	Ala	Leu	Glu	Lys	Ala	Ile	Asn	Phe	Pro	Ser	Phe	Pro	Asp	
	450					455					460					

gct	ttt	aat	tag	1404
Ala	Phe	Asn		
465				

<210> 8
 <211> 467
 <212> PRT
 <213> Agrobacterium tumefaciens

<400> 8
 Met Val Pro Ile Thr Ser Leu Ala Gln Thr Leu Glu Arg Leu Arg Arg
 1 5 10 15
 Lys Asp Tyr Ser Cys Leu Glu Leu Val Glu Thr Leu Ile Ala Arg Cys
 20 25 30
 Gln Ala Ala Lys Pro Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Gly
 35 40 45
 Leu Arg Arg Ser Ala Lys Lys Ile Asp Arg His Gly Asn Ala Gly Leu
 50 55 60
 Gly Leu Cys Gly Ile Pro Leu Cys Phe Lys Ala Asn Ile Ala Thr Gly
 65 70 75 80
 Ile Phe Pro Thr Ser Ala Ala Thr Pro Ala Leu Ile Asn His Leu Pro
 85 90 95
 Lys Ile Pro Ser Arg Val Ala Glu Arg Leu Phe Ser Ala Gly Ala Leu
 100 105 110
 Pro Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser
 115 120 125
 Asn Asn Tyr Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu
 130 135 140
 Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Val Ala Ser Arg
 145 150 155 160
 Leu Met Leu Gly Gly Ile Gly Thr Asp Thr Gly Ala Ser Val Arg Leu
 165 170 175
 Pro Ala Ala Leu Cys Gly Val Val Gly Phe Arg Pro Thr Leu Ala Arg
 180 185 190
 Tyr Pro Arg Asp Arg Ile Ile Pro Val Ser Pro Thr Arg Asp Thr Ala
 195 200 205
 Gly Ile Ile Ala Gln Cys Val Ala Asp Val Ile Ile Leu Asp Gln Val
 210 215 220
 Ile Ser Gly Arg Ser Ala Lys Ile Ser Pro Met Pro Leu Lys Gly Leu
 225 230 235 240
 Arg Ile Gly Leu Pro Thr Thr Tyr Phe Tyr Asp Asp Leu Asp Ala Asp
 245 250 255

sequence listing

Val Ala Phe Ala Ala Glu Thr Thr Ile Arg Leu Leu Ala Asn Arg Gly
 260 265 270
 Val Thr Phe Val Glu Ala Asp Ile Pro His Leu Glu Glu Leu Asn Ser
 275 280 285
 Gly Ala Ser Leu Pro Ile Ala Leu Tyr Glu Phe Pro His Ala Leu Lys
 290 295 300
 Lys Tyr Leu Asp Asp Phe Val Gly Thr Val Ser Phe Ser Asp Val Ile
 305 310 315 320
 Lys Gly Ile Arg Ser Pro Asp Val Ala Asn Ile Val Ser Ala Gln Ile
 325 330 335
 Asp Gly His Gln Ile Ser Asn Asp Glu Tyr Glu Leu Ala Arg Gln Ser
 340 345 350
 Phe Arg Pro Arg Leu Gln Ala Thr Tyr Arg Asn Tyr Phe Arg Leu Tyr
 355 360 365
 Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Ala Ala Lys Ala
 370 375 380
 Ile Gly Gln Glu Ser Ser Val Ile His Asn Gly Ser Met Met Asn Thr
 385 390 395 400
 Phe Lys Ile Tyr Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu
 405 410 415
 Pro Gly Leu Ser Leu Pro Ala Cys Leu Thr Pro Asp Arg Leu Pro Val
 420 425 430
 Gly Met Glu Ile Asp Gly Leu Ala Gly Ser Asp His Arg Leu Leu Ala
 435 440 445
 Ile Gly Ala Ala Leu Glu Lys Ala Ile Asn Phe Pro Ser Phe Pro Asp
 450 455 460
 Ala Phe Asn
 465

<210> 9
 <211> 1404
 <212> DNA
 <213> Agrobacterium tumefaciens
 <220>
 <221> CDS
 <222> (1)..(1401)
 <223> coding for indoleacetamide hydrolase (tms2)

<400> 9
 atg gtg ccc att acc tcg tta gca caa acc cta gaa cgc ctg aga cgg 48
 Met Val Pro Ile Thr Ser Leu Ala Gln Thr Leu Glu Arg Leu Arg Arg
 1 5 10 15
 aaa gac tac tcc tgc tta gaa cta gta gaa act ctg ata gcg cgt tgc 96
 Lys Asp Tyr Ser Cys Leu Glu Leu Val Glu Thr Leu Ile Ala Arg Cys
 20 25 30
 caa gct gca aaa cca tta aat gcc ctt ctg gct aca gac tgg gat ggc 144
 Gln Ala Ala Lys Pro Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Gly
 35 40 45

sequence listing

ttg cgg cga agc gcc aaa aaa att gat cgt cat gga aac gcc gga tta	192
Leu Arg 50 Arg Ser Ala Lys 55 Ile Asp Arg His Gly 60 Asn Ala Gly Leu	
ggt ctt tgc ggc att cca ctc tgt ttt aag gcg aac atc gcg acc ggc	240
Gly 65 Leu Cys Gly Ile Pro 70 Leu Cys Phe Lys 75 Ala Asn Ile Ala Thr Gly 80	
ata ttt cct aca agc gct gct act ccg gcg ctg ata aac cac ttg cca	288
Ile Phe Pro Thr Ser 85 Ala Ala Thr Pro 90 Ala Leu Ile Asn His 95 Leu Pro	
aag ata cca tcc cgc gtc gca gaa aga ctt ttt tca gct gga gca ctg	336
Lys Ile Pro 100 Ser Arg Val Ala Glu Arg 105 Leu Phe Ser Ala 110 Gly Ala Leu	
ccg ggt gcc tcg gga aac atg cat gag tta tcg ttt gga att acg agc	384
Pro Gly 115 Ser Gly Asn Met His 120 Glu Leu Ser Phe Gly 125 Ile Thr Ser	
aac aac tat gcc acc ggt gcg gtg cgg aac ccg tgg aat cca agt ctg	432
Asn Asn 130 Tyr Ala Thr Gly 135 Val Arg Asn Pro 140 Trp Asn Pro Ser Leu	
ata cca gga ggc tca agc ggt ggt gtg gct gct gcg gtg gca agc cga	480
Ile Pro Gly Gly Ser 150 Gly Gly Val Ala 155 Ala Val Ala Ser Arg 160	
ttg atg tta ggc ggc ata ggc acc gat acc ggt gca tct gtt cgc cta	528
Leu Met Leu Gly Gly Ile Gly Thr Asp Thr 170 Gly Ala Ser Val Arg 175 Leu	
ccc gca gcc ctg tgt ggc gta gta gga ttt cga ccg acg ctt gct cga	576
Pro Ala Ala 180 Leu Cys Gly Val Val 185 Gly Phe Arg Pro Thr 190 Leu Ala Arg	
tat cca aga gat cgg ata ata ccg gtc agc ccc acc cgg gac acc gcc	624
Tyr Pro Arg 195 Asp Arg Ile Ile Pro 200 Val Ser Pro Thr Arg 205 Asp Thr Ala	
gga atc ata gcg cag tgc gta gcc gat gtt ata atc ctc gat cag gtg	672
Gly Ile Ile Ala Gln Cys Val 215 Ala Asp Val Ile 220 Ile Leu Asp Gln Val	
att tcc gga cgg tcg gcg aaa att tca ccc atg ccg ctg aag ggg ctt	720
Ile Ser Gly Arg Ser 230 Lys Ile Ser Pro 235 Met Pro Leu Lys Gly 240 Leu	
cgg atc ggc ctc ccc act acc tac ttt tac gat gac ctt gat gct gat	768
Arg Ile Gly Leu Pro 245 Thr Thr Tyr Phe Tyr 250 Asp Asp Leu Asp Ala 255 Asp	
gtg gcc ttc gca gct gaa acg acg att cgc ttg cta gcc aac aga ggc	816
Val Ala Phe 260 Ala Ala Glu Thr Thr 265 Arg Leu Leu Ala Asn Arg Gly	
gta acc ttt gtt gaa gcc gac atc ccc cac cta gag gaa ctg aat agt	864
Val Thr 275 Val Glu Ala Asp Ile 280 Pro His Leu Glu 285 Glu Leu Asn Ser	
ggg gca agt ttg cca att gcg ctt tac gaa ttt cca cac gct cta aaa	912
Gly Ala Ser Leu Pro Ile 295 Ala Leu Tyr Glu Phe Pro 300 His Ala Leu Lys	

sequence listing

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aag tat ctc gac gat ttt gtg gga aca gtt tct ttt tct gac gtt atc 960
Lys Tyr Leu Asp Asp Phe Val Gly Thr Val Ser Phe Ser Asp Val Ile
305 310 315 320

aaa gga att cgt agc ccc gat gta gcg aac att gtc agt gcg caa att 1008
Lys Gly Ile Arg Ser Pro Asp Val Ala Asn Ile Val Ser Ala Gln Ile
325 330 335

gat ggg cat caa att tcc aac gat gaa tat gaa ctg gcg cgt caa tcc 1056
Asp Gly His Gln Ile Ser Asn Asp Glu Tyr Glu Leu Ala Arg Gln Ser
340 345 350

ttc agg cca agg ctc cag gcc act tat cgg aat tac ttc aga ctc tat 1104
Phe Arg Pro Arg Leu Gln Ala Thr Tyr Arg Asn Tyr Phe Arg Leu Tyr
355 360 365

cag tta gat gca atc ctt ttc cca act gca ccc tta gcg gcc aaa gcc 1152
Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Ala Ala Lys Ala
370 375 380

ata ggt cag gag tcg tca gtc atc cac aat ggc tca atg ata aac act 1200
Ile Gly Gln Glu Ser Val Ile His Asn Gly Ser Met Ile Asn Thr
385 390 395 400

ttc aag atc tac gtg cga aat gtg gac cca agc agc aac gca ggc cta 1248
Phe Lys Ile Tyr Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu
405 410 415

cct ggg ttg agc ctt cct gcc tgc ctt aca cct gat cgc ttg cct gtt 1296
Pro Gly Leu Ser Leu Pro Ala Cys Leu Thr Pro Asp Arg Leu Pro Val
420 425 430

gga atg gaa att gac gga tta gcg ggg tca gac cac cgt ctg tta gca 1344
Gly Met Glu Ile Asp Gly Leu Ala Gly Ser Asp His Arg Leu Leu Ala
435 440 445

atc ggg gca gca tta gaa aaa gcc ata aat ttt cct tcc ttt ccc gat 1392
Ile Gly Ala Ala Leu Glu Lys Ala Ile Asn Phe Pro Ser Phe Pro Asp
450 455 460

gct ttt aat tag 1404
Ala Phe Asn
465

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<210> 10

<211> 467

<212> PRT

<213> Agrobacterium tumefaciens

<400> 10

Met Val Pro Ile Thr Ser Leu Ala Gln Thr Leu Glu Arg Leu Arg Arg
1 5 10 15

Lys Asp Tyr Ser Cys Leu Glu Leu Val Glu Thr Leu Ile Ala Arg Cys
20 25 30

Gln Ala Ala Lys Pro Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Gly
35 40 45

Leu Arg Arg Ser Ala Lys Lys Ile Asp Arg His Gly Asn Ala Gly Leu
50 55 60

sequence listing

Gly 65 Leu Cys Gly Ile Pro 70 Leu Cys Phe Lys Ala 75 Asn Ile Ala Thr Gly 80
 Ile Phe Pro Thr Ser 85 Ala Ala Thr Pro Ala 90 Leu Ile Asn His Leu Pro 95
 Lys Ile Pro Ser Arg Val Ala Glu Arg 105 Leu Phe Ser Ala Gly 110 Ala Leu
 Pro Gly Ala 115 Ser Gly Asn Met His 120 Glu Leu Ser Phe Gly 125 Ile Thr Ser
 Asn Asn Tyr Ala Thr Gly Ala 135 Val Arg Asn Pro Trp Asn Pro Ser Leu 140
 Ile Pro Gly Gly Ser Ser 150 Gly Gly Val Ala Ala 155 Ala Val Ala Ser Arg 160
 Leu Met Leu Gly Gly 165 Ile Gly Thr Asp Thr 170 Gly Ala Ser Val Arg 175 Leu
 Pro Ala Ala Leu 180 Cys Gly Val Val Gly 185 Phe Arg Pro Thr Leu 190 Ala Arg
 Tyr Pro Arg Asp Arg Ile Ile Pro 200 Val Ser Pro Thr Arg 205 Asp Thr Ala
 Gly Ile Ile Ala Gln Cys Val 215 Ala Asp Val Ile Ile 220 Leu Asp Gln Val
 Ile Ser Gly Arg Ser Ala 230 Lys Ile Ser Pro Met 235 Pro Leu Lys Gly Leu 240
 Arg Ile Gly Leu Pro 245 Thr Thr Tyr Phe Tyr 250 Asp Asp Leu Asp Ala 255 Asp
 Val Ala Phe Ala 260 Ala Glu Thr Thr Ile 265 Arg Leu Leu Ala Asn Arg Gly 270
 Val Thr Phe Val Glu Ala Asp Ile 280 Pro His Leu Glu Glu 285 Leu Asn Ser
 Gly Ala Ser Leu Pro Ile Ala 295 Leu Tyr Glu Phe Pro 300 His Ala Leu Lys
 Lys Tyr Leu Asp Asp Phe 310 Val Gly Thr Val Ser 315 Phe Ser Asp Val Ile 320
 Lys Gly Ile Arg Ser 325 Pro Asp Val Ala Asn 330 Ile Val Ser Ala Gln Ile 335
 Asp Gly His Gln 340 Ile Ser Asn Asp Glu 345 Tyr Glu Leu Ala Arg 350 Gln Ser
 Phe Arg Pro Arg Leu Gln Ala Thr 360 Tyr Arg Asn Tyr Phe 365 Arg Leu Tyr
 Gln Leu Asp Ala Ile Leu Phe 375 Pro Thr Ala Pro Leu 380 Ala Ala Lys Ala
 Ile Gly Gln Glu Ser Ser 390 Val Ile His Asn Gly 395 Ser Met Ile Asn Thr 400

sequence listing

Phe Lys Ile Tyr Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu
405 410 415
Pro Gly Leu Ser Leu Pro Ala Cys Leu Thr Pro Asp Arg Leu Pro Val
420 425 430
Gly Met Glu Ile Asp Gly Leu Ala Gly Ser Asp His Arg Leu Leu Ala
435 440 445
Ile Gly Ala Ala Leu Glu Lys Ala Ile Asn Phe Pro Ser Phe Pro Asp
450 455 460
Ala Phe Asn
465

<210> 11

<211> 609

<212> DNA

<213> Xanthobacter autotrophicus

<220>

<221> CDS

<222> (1)..(603)

<223> coding for haloalkane dehalogenase

<400> 11

atg tca acg ttt ttt gaa ccg gag aac gga atg aaa caa aac gcc aaa 48
Met Ser Thr Phe Phe Glu Pro Glu Asn Gly Met Lys Gln Asn Ala Lys
1 5 10 15

acc gaa cga atc ctg gat gtc gcg ctc gaa ttg ctt gag aca gag ggt 96
Thr Glu Arg Ile Leu Asp Val Ala Leu Glu Leu Leu Glu Thr Glu Gly
20 25 30

gag ttt ggt ttg acg atg agg cag gtg gca acg caa gcg gac atg tcc 144
Glu Phe Gly Leu Thr Met Arg Gln Val Ala Thr Gln Ala Asp Met Ser
35 40 45

ctg agc aac gtt cag tac tat ttc aag tcc gag gac ctg ctc ctc gtg 192
Leu Ser Asn Val Gln Tyr Tyr Phe Lys Ser Glu Asp Leu Leu Leu Val
50 55 60

gcc atg gca gac cgt tac ttt caa cgg tgc ctg aca acc atg gct gag 240
Ala Met Ala Asp Arg Tyr Phe Gln Arg Cys Leu Thr Thr Met Ala Glu
65 70 75 80

cat ccg ccc tta tcg gca ggg cgt gat caa cac gcc cag tta aga gcg 288
His Pro Pro Leu Ser Ala Gly Arg Asp Gln His Ala Gln Leu Arg Ala
85 90 95

ttg tta cga gaa ctg ctc ggt cat ggt ctt gag att tcc gag atg tgt 336
Leu Leu Arg Glu Leu Leu Gly His Gly Leu Glu Ile Ser Glu Met Cys
100 105 110

cga ata ttc agg gag tac tgg gca atc gcc acc cgt aat gaa act gtt 384
Arg Ile Phe Arg Glu Tyr Trp Ala Ile Ala Thr Arg Asn Glu Thr Val
115 120 125

cac ggc tat ctc aag tcg tac tat cgg gat ctc gcc gaa gtg atg gct 432
His Gly Tyr Leu Lys Ser Tyr Tyr Arg Asp Leu Ala Glu Val Met Ala
130 135 140

gag aag ctt gcg cca ctg gcc agc agc gaa aag gcg ctg gcc gtg gcc 480

sequence listing

Glu	Lys	Leu	Ala	Pro	Leu	Ala	Ser	Ser	Glu	Lys	Ala	Leu	Ala	Val	Ala		
145					150				155						160		
gta	tct	ttg	gtt	att	cct	tat	gtt	gag	ggg	tat	tcg	gta	acg	gcc	att		528
Val	Ser	Leu	Val	Ile	Pro	Tyr	Val	Glu	Gly	Tyr	Ser	Val	Thr	Ala	Ile		
				165					170					175			
gca	atg	ccc	gaa	tcc	att	gat	acg	att	tcc	gag	acg	ctg	acc	aat	gtg		576
Ala	Met	Pro	Glu	Ser	Ile	Asp	Thr	Ile	Ser	Glu	Thr	Leu	Thr	Asn	Val		
			180					185					190				
gtg	ttg	gag	cag	ctt	cgc	atc	agc	aat	tcatga								609
Val	Leu	Glu	Gln	Leu	Arg	Ile	Ser	Asn									
		195				200											

<210> 12
 <211> 201
 <212> PRT
 <213> Xanthobacter autotrophicus

<400> 12
 Met Ser Thr Phe Phe Glu Pro Glu Asn Gly Met Lys Gln Asn Ala Lys
 1 5 10 15
 Thr Glu Arg Ile Leu Asp Val Ala Leu Glu Leu Leu Glu Thr Glu Gly
 20 25 30
 Glu Phe Gly Leu Thr Met Arg Gln Val Ala Thr Gln Ala Asp Met Ser
 35 40 45
 Leu Ser Asn Val Gln Tyr Tyr Phe Lys Ser Glu Asp Leu Leu Leu Val
 50 55 60
 Ala Met Ala Asp Arg Tyr Phe Gln Arg Cys Leu Thr Thr Met Ala Glu
 65 70 75 80
 His Pro Pro Leu Ser Ala Gly Arg Asp Gln His Ala Gln Leu Arg Ala
 85 90 95
 Leu Leu Arg Glu Leu Leu Gly His Gly Leu Glu Ile Ser Glu Met Cys
 100 105 110
 Arg Ile Phe Arg Glu Tyr Trp Ala Ile Ala Thr Arg Asn Glu Thr Val
 115 120 125
 His Gly Tyr Leu Lys Ser Tyr Tyr Arg Asp Leu Ala Glu Val Met Ala
 130 135 140
 Glu Lys Leu Ala Pro Leu Ala Ser Ser Glu Lys Ala Leu Ala Val Ala
 145 150 155 160
 Val Ser Leu Val Ile Pro Tyr Val Glu Gly Tyr Ser Val Thr Ala Ile
 165 170 175
 Ala Met Pro Glu Ser Ile Asp Thr Ile Ser Glu Thr Leu Thr Asn Val
 180 185 190
 Val Leu Glu Gln Leu Arg Ile Ser Asn
 195 200

<210> 13
 <211> 1131
 <212> DNA

sequence listing

<213> Herpes simplex virus 1

<220>

<221> CDS

<222> (1)..(1128)

<223> coding for thymidine kinase (TK)

<400> 13

atg gct tcg tac ccc tgc cat caa cac gcg tct gcg ttc gac cag gct	48
Met Ala Ser Tyr Pro Cys His Gln His Ala Ser Ala Phe Asp Gln Ala	
1 5 10 15	
gcg cgt tct cgc ggc cat agc aac cga cgt acg gcg ttg cgc cct cgc	96
Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr Ala Leu Arg Pro Arg	
20 25 30	
cgg cag caa gaa gcc acg gaa gtc cgc ctg gag cag aaa atg ccc acg	144
Arg Gln Gln Glu Ala Thr Glu Val Arg Leu Glu Gln Lys Met Pro Thr	
35 40 45	
cta ctg cgg gtt tat ata gac ggt cct cac ggg atg ggg aaa acc acc	192
Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr	
50 55 60	
acc acg caa ctg ctg gtg gcc ctg ggt tcg cgc gac gat atc gtc tac	240
Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr	
65 70 75 80	
gta ccc gag ccg atg act tac tgg cag gtg ctg ggg gct tcc gag aca	288
Val Pro Glu Pro Met Thr Tyr Trp Gln Val Leu Gly Ala Ser Glu Thr	
85 90 95	
atc gcg aac atc tac acc aca caa cac cgc ctc gac cag ggt gag ata	336
Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile	
100 105 110	
tcg gcc ggg gac gcg gcg gtg gta atg aca agc gcc cag ata aca atg	384
Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met	
115 120 125	
ggc atg cct tat gcc gtg acc gac gcc gtt ctg gct cct cat gtc ggg	432
Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Val Gly	
130 135 140	
ggg gag gct ggg agt tca cat gcc ccg ccc ccg gcc ctc acc ctc atc	480
Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile	
145 150 155 160	
ttc gac cgc cat ccc atc gcc gcc ctc ctg tgc tac ccg gcc gcg cga	528
Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg	
165 170 175	
tac ctt atg ggc agc atg acc ccc cag gcc gtg ctg gcg ttc gtg gcc	576
Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala	
180 185 190	
ctc atc ccg ccg acc ttg ccc ggc aca aac atc gtg ttg ggg gcc ctt	624
Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu	
195 200 205	
ccg gag gac aga cac atc gac cgc ctg gcc aaa cgc cag cgc ccc ggc	672
Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly	
210 215 220	

sequence listing

gag cgg ctt gac ctg gct atg ctg gcc gcg att cgc cgc gtt tac ggg Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly 225 230 235 240	720
ctg ctt gcc aat acg gtg cgg tat ctg cag ggc ggc ggc tcg tgg tgg Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Gly Gly Gly Ser Trp Trp 245 250 255	768
gag gat tgg gga cag ctt tcg ggg acg gcc gtg ccg ccc cag ggt gcc Glu Asp Trp Gly Gln Leu Ser Gly Thr Ala Val Pro Pro Gln Gly Ala 260 265 270	816
gag ccc cag agc aac gcg ggc cca cga ccc cat atc ggg gac acg tta Glu Pro Gln Ser Asn Ala Gly Pro Arg Pro His Ile Gly Asp Thr Leu 275 280 285	864
ttt acc ctg ttt cgg gcc ccc gag ttg ctg gcc ccc aac ggc gac ctg Phe Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala Pro Asn Gly Asp Leu 290 295 300	912
tat aac gtg ttt gcc tgg gcc ttg gac gtc ttg gcc aaa cgc ctc cgt Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu Ala Lys Arg Leu Arg 305 310 315 320	960
ccc atg cac gtc ttt atc ctg gat tac gac caa tcg ccc gcc ggc tgc Pro Met His Val Phe Ile Leu Asp Tyr Asp Gln Ser Pro Ala Gly Cys 325 330 335	1008
cgg gac gcc ctg ctg caa ctt acc tcc ggg atg gtc cag acc cac gtc Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met Val Gln Thr His Val 340 345 350	1056
acc acc cca ggc tcc ata ccg acg atc tgc gac ctg gcg cgc acg ttt Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp Leu Ala Arg Thr Phe 355 360 365	1104
gcc cgg gag atg ggg gag gct aac tga Ala Arg Glu Met Gly Glu Ala Asn 370 375	1131

<210> 14

<211> 376

<212> PRT

<213> Herpes simplex virus 1

<400> 14

Met Ala Ser Tyr Pro Cys His Gln His Ala Ser Ala Phe Asp Gln Ala
1 5 10 15

Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr Ala Leu Arg Pro Arg
20 25 30

Arg Gln Gln Glu Ala Thr Glu Val Arg Leu Glu Gln Lys Met Pro Thr
35 40 45

Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr
50 55 60

Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr
65 70 75 80

Val Pro Glu Pro Met Thr Tyr Trp Gln Val Leu Gly Ala Ser Glu Thr
85 90 95

sequence listing

```

Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile
      100      105      110
Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met
      115      120      125
Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Val Gly
      130      135      140
Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile
      145      150      155      160
Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg
      165      170      175
Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala
      180      185      190
Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu
      195      200      205
Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly
      210      215      220
Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly
      225      230      235      240
Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Gly Gly Gly Ser Trp Trp
      245      250      255
Glu Asp Trp Gly Gln Leu Ser Gly Thr Ala Val Pro Pro Gln Gly Ala
      260      265      270
Glu Pro Gln Ser Asn Ala Gly Pro Arg Pro His Ile Gly Asp Thr Leu
      275      280      285
Phe Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala Pro Asn Gly Asp Leu
      290      295      300
Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu Ala Lys Arg Leu Arg
      305      310      315      320
Pro Met His Val Phe Ile Leu Asp Tyr Asp Gln Ser Pro Ala Gly Cys
      325      330      335
Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met Val Gln Thr His Val
      340      345      350
Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp Leu Ala Arg Thr Phe
      355      360      365
Ala Arg Glu Met Gly Glu Ala Asn
      370      375

```

```

<210> 15
<211> 1131
<212> DNA
<213> Herpes simplex virus 1
<220>
<221> CDS
<222> (1)..(1128)

```

sequence listing

<223> coding for thymidine kinase (TK)

```

<400> 15
atg gct tcg tac ccc tgc cat caa cac gcg tct gcg ttc gac cag gct 48
Met Ala Ser Tyr Pro Cys His Gln His Ala Ser Ala Phe Asp Gln Ala
1 5 10 15

gcg cgt tct cgc ggc cat agc aac cga cgt acg gcg ttg cgc cct cgc 96
Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr Ala Leu Arg Pro Arg
20 25 30

cgg cag caa gaa gcc acg gaa gtc cgc ctg gag cag aaa atg ccc acg 144
Arg Gln Gln Glu Ala Thr Glu Val Arg Leu Glu Gln Lys Met Pro Thr
35 40 45

cta ctg cgg gtt tat ata gac ggt cct cac ggg atg ggg aaa acc acc 192
Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr
50 55 60

acc acg caa ctg ctg gtg gcc ctg ggt tcg cgc gac gat atc gtc tac 240
Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr
65 70 75 80

gta ccc gag ccg atg act tac tgg cag gtg ctg ggg gct tcc gag aca 288
Val Pro Glu Pro Met Thr Tyr Trp Gln Val Leu Gly Ala Ser Glu Thr
85 90 95

atc gcg aac atc tac acc aca caa cac cgc ctc gac cag ggt gag ata 336
Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile
100 105 110

tcg gcc ggg gac gcg gcg gtg gta atg aca agc gcc cag ata aca atg 384
Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met
115 120 125

ggc atg cct tat gcc gtg acc gac gcc gtt ctg gct cct cat gtc ggg 432
Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Val Gly
130 135 140

ggg gag gct ggg agt tca cat gcc ccg ccc ccg gcc ctc acc ctc atc 480
Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile
145 150 155 160

ttc gac cgc cat ccc atc gcc gcc ctc ctg tgc tac ccg gcc gcg cga 528
Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg
165 170 175

tac ctt atg ggc agc atg acc ccc cag gcc gtg ctg gcg ttc gtg gcc 576
Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala
180 185 190

ctc atc ccg ccg acc ttg ccc ggc aca aac atc gtg ttg ggg gcc ctt 624
Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu
195 200 205

ccg gag gac aga cac atc gac cgc ctg gcc aaa cgc cag cgc ccc ggc 672
Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly
210 215 220

gag cgg ctt gac ctg gct atg ctg gcc gcg att cgc cgc gtt tac ggg 720
Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly
225 230 235 240

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sequence listing

ctg	ctt	gcc	aat	acg	gtg	cgg	tat	ctg	cag	ggc	ggc	ggg	tcg	tgg	tgg	768
Leu	Leu	Ala	Asn	Thr	Val	Arg	Tyr	Leu	Gln	Gly	Gly	Gly	Ser	Trp	Trp	
				245					250					255		
gag	gat	tgg	gga	cag	ctt	tcg	ggg	acg	gcc	gtg	ccg	ccc	cag	ggt	gcc	816
Glu	Asp	Trp	Gly	Gln	Leu	Ser	Gly	Thr	Ala	Val	Pro	Pro	Gln	Gly	Ala	
			260					265					270			
gag	ccc	cag	agc	aac	gcg	ggc	cca	cga	ccc	cat	atc	ggg	gac	acg	tta	864
Glu	Pro	Gln	Ser	Asn	Ala	Gly	Pro	Arg	Pro	His	Ile	Gly	Asp	Thr	Leu	
		275					280					285				
ttt	acc	ctg	ttt	cgg	gcc	ccc	gag	ttg	ctg	gcc	ccc	aac	ggc	gac	ctg	912
Phe	Thr	Leu	Phe	Arg	Ala	Pro	Glu	Leu	Leu	Ala	Pro	Asn	Gly	Asp	Leu	
	290					295					300					
tat	aac	gtg	ttt	gcc	tgg	gcc	ttg	gac	gtc	ttg	gcc	aaa	cgc	ctc	cgt	960
Tyr	Asn	Val	Phe	Ala	Trp	Ala	Leu	Asp	Val	Leu	Ala	Lys	Arg	Leu	Arg	
					310					315					320	
ccc	atg	cac	gtc	ttt	atc	ctg	gat	tac	gac	caa	tcg	ccc	gcc	ggc	tgc	1008
Pro	Met	His	Val	Phe	Ile	Leu	Asp	Tyr	Asp	Gln	Ser	Pro	Ala	Gly	Cys	
				325					330					335		
cgg	gac	gcc	ctg	ctg	caa	ctt	acc	tcc	ggg	atg	gtc	cag	acc	cac	gtc	1056
Arg	Asp	Ala	Leu	Leu	Gln	Leu	Thr	Ser	Gly	Met	Val	Gln	Thr	His	Val	
			340					345					350			
acc	acc	cca	ggc	tcc	ata	ccg	acg	atc	tgc	gac	ctg	gcg	cgc	acg	ttt	1104
Thr	Thr	Pro	Gly	Ser	Ile	Pro	Thr	Ile	Cys	Asp	Leu	Ala	Arg	Thr	Phe	
		355					360					365				
gcc	cgg	gag	atg	ggg	gag	gct	aac	tga								1131
Ala	Arg	Glu	Met	Gly	Glu	Ala	Asn									
		370				375										

<210> 16
 <211> 376
 <212> PRT
 <213> Herpes simplex virus 1

<400> 16
 Met Ala Ser Tyr Pro Cys His Gln His Ala Ser Ala Phe Asp Gln Ala
 1 5 10 15
 Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr Ala Leu Arg Pro Arg
 20 25 30
 Arg Gln Gln Glu Ala Thr Glu Val Arg Leu Glu Gln Lys Met Pro Thr
 35 40 45
 Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr
 50 55 60
 Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr
 65 70 75 80
 Val Pro Glu Pro Met Thr Tyr Trp Gln Val Leu Gly Ala Ser Glu Thr
 85 90 95
 Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile
 100 105 110

sequence listing

Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met
115 120

Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Val Gly
130 135 140

Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile
145 150 155 160

Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg
165 170 175

Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala
180 185 190

Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu
195 200 205

Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly
210 215 220

Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly
225 230 235 240

Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Gly Gly Gly Ser Trp Trp
245 250 255

Glu Asp Trp Gly Gln Leu Ser Gly Thr Ala Val Pro Pro Gln Gly Ala
260 265 270

Glu Pro Gln Ser Asn Ala Gly Pro Arg Pro His Ile Gly Asp Thr Leu
275 280 285

Phe Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala Pro Asn Gly Asp Leu
290 295 300

Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu Ala Lys Arg Leu Arg
305 310 315 320

Pro Met His Val Phe Ile Leu Asp Tyr Asp Gln Ser Pro Ala Gly Cys
325 330 335

Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met Val Gln Thr His Val
340 345 350

Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp Leu Ala Arg Thr Phe
355 360 365

Ala Arg Glu Met Gly Glu Ala Asn
370 375

<210> 17
<211> 840
<212> DNA
<213> Toxoplasma gondii
<220>
<221> CDS
<222> (1)..(837)
<223> coding for hypoxanthine-xanthine-guanine
phosphoribosyl transferase (HXGPRTase)

<400> 17
atg gcg tcc aaa ccc att gaa gaa tcc cgg tcg caa aaa cgg agt gcc 48
Page 25

sequence listing																	
Met 1	Ala	Ser	Lys	Pro 5	Ile	Glu	Glu	Ser	Arg 10	Ser	Gln	Lys	Arg	Ser 15	Ala		
ttc Phe	tca Ser	gac Asp	atc Ile 20	ttc Phe	tgt Cys	tgt Cys	tgc Cys	act Thr 25	cct Pro	aat Asn	gaa Glu	ggg Gly 30	gct Ala 30	atc Ile	gtg Val	96	
ccc Pro	agt Ser	gac Asp 35	cca Pro	atg Met	gtc Val	tcc Ser	acc Thr 40	agt Ser	gct Ala	cca Pro	gca Ala	cgc Arg 45	acc Thr	agt Ser	gct Ala	144	
cca Pro	gcg Ala 50	cgc Arg	tcc Ser	agt Ser	gca Ala	ctt Leu 55	caa Gln	gac Asp	tac Tyr	ggc Gly	aag Lys 60	ggc Gly	aag Lys	ggc Gly	cgt Arg	192	
att Ile 65	gag Glu	ccc Pro	atg Met	tat Tyr	atc Ile 70	ccc Pro	gac Asp	aac Asn	acc Thr	ttc Phe 75	tac Tyr	aac Asn	gct Ala	gat Asp	gac Asp 80	240	
ttt Phe	ctt Leu	gtg Val	ccc Pro	ccc Pro 85	cac His	tgc Cys	aag Lys	ccc Pro	tac Tyr 90	att Ile	gac Asp	aaa Lys	atc Ile	ctc Leu 95	ctc Leu	288	
cct Pro	ggt Gly	gga Gly	ttg Leu 100	gtc Val	aag Lys	gac Asp	aga Arg	gtt Val 105	gag Glu	aag Lys	ttg Leu	gcg Ala 110	tat Tyr	gac Asp	atc Ile	336	
cac His	aga Arg	act Thr 115	tac Tyr	ttc Phe	ggc Gly	gag Glu	gag Glu 120	ttg Leu	cac His	atc Ile	att Ile	tgc Cys 125	atc Ile	ctg Leu	aaa Lys	384	
ggc Gly	tct Ser 130	cgc Arg	ggc Gly	ttc Phe	ttc Phe	aac Asn 135	ctt Leu	ctg Leu	atc Ile	gac Asp	tac Tyr 140	ctt Leu	gcc Ala	acc Thr	ata Ile	432	
cag Gln 145	aag Lys	tac Tyr	agt Ser	ggt Gly	cgt Arg 150	gag Glu	tcc Ser	agc Ser	gtg Val	ccc Pro 155	ccc Pro	ttc Phe	ttc Phe	gag Glu	cac His 160	480	
tat Tyr	gtc Val	cgc Arg	ctg Leu	aag Lys 165	tcc Ser	tac Tyr	cag Gln	aac Asn	gac Asp 170	aac Asn	agc Ser	aca Thr	ggc Gly	cag Gln 175	ctc Leu	528	
acc Thr	gtc Val	ttg Leu	agc Ser 180	gac Asp	gac Asp	ttg Leu	tca Ser	atc Ile 185	ttt Phe	cgc Arg	gac Asp	aag Lys	cac His 190	gtt Val	ctg Leu	576	
att Ile	gtt Val	gag Glu 195	gac Asp	atc Ile	gtc Val	gac Asp	acc Thr 200	ggt Gly	ttc Phe	acc Thr	ctc Leu	acc Thr 205	gag Glu	ttc Phe	ggt Gly	624	
gag Glu	cgc Arg 210	ctg Leu	aaa Lys	gcc Ala	gtc Val	ggt Gly 215	ccc Pro	aag Lys	tcg Ser	atg Met	aga Arg 220	atc Ile	gcc Ala	acc Thr	ctc Leu	672	
gtc Val 225	gag Glu	aag Lys	cgc Arg	aca Thr	gat Asp 230	cgc Arg	tcc Ser	aac Asn	agc Ser	ttg Leu 235	aag Lys	ggc Gly	gac Asp	ttc Phe	gtc Val 240	720	
ggc Gly	ttc Phe	agc Ser	att Ile	gaa Glu 245	gac Asp	gtc Val	tgg Trp	atc Ile	gtt Val 250	ggt Gly	tgc Cys	tgc Cys	tac Tyr	gac Asp 255	ttc Phe	768	

sequence listing

aac gag atg ttc cgc gac ttc gac cac gtc gcc gtc ctg agc gac gcc	816
Asn Glu Met Phe Arg Asp Phe Asp His Val Ala Val Leu Ser Asp Ala	
260 265 270	

gct cgc aaa aag ttc gag aag taa	840
Ala Arg Lys Lys Phe Glu Lys	
275	

<210> 18
 <211> 279
 <212> PRT
 <213> Toxoplasma gondii

<400> 18
 Met Ala Ser Lys Pro Ile Glu Glu Ser Arg Ser Gln Lys Arg Ser Ala
 1 5 10 15
 Phe Ser Asp Ile Phe Cys Cys Cys Thr Pro Asn Glu Gly Ala Ile Val
 20 25 30
 Pro Ser Asp Pro Met Val Ser Thr Ser Ala Pro Ala Arg Thr Ser Ala
 35 40 45
 Pro Ala Arg Ser Ser Ala Leu Gln Asp Tyr Gly Lys Gly Lys Gly Arg
 50 55 60
 Ile Glu Pro Met Tyr Ile Pro Asp Asn Thr Phe Tyr Asn Ala Asp Asp
 65 70 75 80
 Phe Leu Val Pro Pro His Cys Lys Pro Tyr Ile Asp Lys Ile Leu Leu
 85 90 95
 Pro Gly Gly Leu Val Lys Asp Arg Val Glu Lys Leu Ala Tyr Asp Ile
 100 105 110
 His Arg Thr Tyr Phe Gly Glu Glu Leu His Ile Ile Cys Ile Leu Lys
 115 120 125
 Gly Ser Arg Gly Phe Phe Asn Leu Leu Ile Asp Tyr Leu Ala Thr Ile
 130 135 140
 Gln Lys Tyr Ser Gly Arg Glu Ser Ser Val Pro Pro Phe Phe Glu His
 145 150 155 160
 Tyr Val Arg Leu Lys Ser Tyr Gln Asn Asp Asn Ser Thr Gly Gln Leu
 165 170 175
 Thr Val Leu Ser Asp Asp Leu Ser Ile Phe Arg Asp Lys His Val Leu
 180 185 190
 Ile Val Glu Asp Ile Val Asp Thr Gly Phe Thr Leu Thr Glu Phe Gly
 195 200 205
 Glu Arg Leu Lys Ala Val Gly Pro Lys Ser Met Arg Ile Ala Thr Leu
 210 215 220
 Val Glu Lys Arg Thr Asp Arg Ser Asn Ser Leu Lys Gly Asp Phe Val
 225 230 235 240
 Gly Phe Ser Ile Glu Asp Val Trp Ile Val Gly Cys Cys Tyr Asp Phe
 245 250 255

sequence listing

Asn Glu Met Phe Arg Asp Phe Asp His Val Ala Val Leu Ser Asp Ala
 260 265 270

Ala Arg Lys Lys Phe Glu Lys
 275

<210> 19
 <211> 459
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)..(456)
 <223> coding for xanthine-guanine phosphoribosyl
 transferase (gpt)

<400> 19
 atg agc gaa aaa tac atc gtc acc tgg gac atg ttg cag atc cat gca 48
 Met Ser Glu Lys Tyr 5 Ile Val Thr Trp Asp Met Leu Gln Ile His Ala
 1 5 10 15
 cgt aaa ctc gca agc cga ctg atg cct tct gaa caa tgg aaa ggc att 96
 Arg Lys Leu Ala Ser Arg Leu Met Pro Ser Glu Gln Trp Lys Gly Ile
 20 25 30
 att gcc gta agc cgt ggc ggt ctg gta ccg ggt gcg tta ctg gcg cgt 144
 Ile Ala Val Ser Arg Gly Gly Leu Val Pro Gly Ala Leu Leu Ala Arg
 35 40 45
 gaa ctg ggt att cgt cat gtc gat acc gtt tgt att tcc agc tac gat 192
 Glu Leu Gly Ile Arg His Val Asp Thr Val Cys Ile Ser Ser Tyr Asp
 50 55 60
 cac gac aac cag cgc gag ctt aaa gtg ctg aaa cgc gca gaa ggc gat 240
 His Asp Asn Gln Arg Glu Leu Lys Val Leu Lys Arg Ala Glu Gly Asp
 65 70 75 80
 ggc gaa ggc ttc atc gtt att gat gac ctg gtg gat acc ggt ggt act 288
 Gly Glu Gly Phe Ile Val Ile Asp Asp Leu Val Asp Thr Gly Gly Thr
 85 90
 gcg gtt gcg att cgt gaa atg tat cca aaa gcg cac ttt gtc acc atc 336
 Ala Val Ala Ile Arg Glu Met Tyr Pro Lys Ala His Phe Val Thr Ile
 100 105 110
 ttc gca aaa ccg gct ggt cgt ccg ctg gtt gat gac tat gtt gtt gat 384
 Phe Ala Lys Pro Ala Gly Arg Pro Leu Val Asp Asp Tyr Val Val Asp
 115 120
 atc ccg caa gat acc tgg att gaa cag ccg tgg gat atg ggc gtc gta 432
 Ile Pro Gln Asp Thr Trp Ile Glu Gln Pro Trp Asp Met Gly Val Val
 130 135 140
 ttc gtc ccg cca atc tcc ggt cgc taa 459
 Phe Val Pro Pro Ile Ser Gly Arg
 145 150

<210> 20
 <211> 152
 <212> PRT
 <213> Escherichia coli

sequence listing

<400> 20

Met Ser Glu Lys Tyr Ile Val Thr Trp Asp Met Leu Gln Ile His Ala
1 5 10 15

Arg Lys Leu Ala Ser Arg Leu Met Pro Ser Glu Gln Trp Lys Gly Ile
20 25 30

Ile Ala Val Ser Arg Gly Gly Leu Val Pro Gly Ala Leu Leu Ala Arg
35 40 45

Glu Leu Gly Ile Arg His Val Asp Thr Val Cys Ile Ser Ser Tyr Asp
50 55 60

His Asp Asn Gln Arg Glu Leu Lys Val Leu Lys Arg Ala Glu Gly Asp
65 70 75 80

Gly Glu Gly Phe Ile Val Ile Asp Asp Leu Val Asp Thr Gly Gly Thr
85 90 95

Ala Val Ala Ile Arg Glu Met Tyr Pro Lys Ala His Phe Val Thr Ile
100 105 110

Phe Ala Lys Pro Ala Gly Arg Pro Leu Val Asp Asp Tyr Val Val Asp
115 120 125

Ile Pro Gln Asp Thr Trp Ile Glu Gln Pro Trp Asp Met Gly Val Val
130 135 140

Phe Val Pro Pro Ile Ser Gly Arg
145 150

<210> 21

<211> 459

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(456)

<223> coding for xanthine-guanine phosphoribosyl
transferase (gpt)

<400> 21

atg agc gaa aaa tac atc gtc acc tgg gac atg ttg cag atc cat gca 48
Met Ser Glu Lys Tyr Ile Val Thr Trp Asp Met Leu Gln Ile His Ala
1 5 10 15

cgt aaa ctc gca agc cga ctg atg cct tct gaa caa tgg aaa ggc att 96
Arg Lys Leu Ala Ser Arg Leu Met Pro Ser Glu Gln Trp Lys Gly Ile
20 25 30

att gcc gta agc cgt ggc ggt ctg gta ccg ggt gcg tta ctg gcg cgt 144
Ile Ala Val Ser Arg Gly Gly Leu Val Pro Gly Ala Leu Leu Ala Arg
35 40 45

gaa ctg ggt att cgt cat gtc gat acc gtt tgt att tcc agc tac gat 192
Glu Leu Gly Ile Arg His Val Asp Thr Val Cys Ile Ser Ser Tyr Asp
50 55 60

cac gac aac cag cgc gag ctt aaa gtg ctg aaa cgc gca gaa ggc gat 240
His Asp Asn Gln Arg Glu Leu Lys Val Leu Lys Arg Ala Glu Gly Asp
65 70 75 80

sequence listing

ggc gaa ggc ttc atc gtt att gat gac ctg gtg gat acc ggt ggt act 288
Gly Glu Gly Phe Ile Val Ile Asp Asp Leu Val Asp Thr Gly Gly Thr
85 90 95

gcg gtt gcg att cgt gaa atg tat cca aaa gcg cac ttt gtc acc atc 336
Ala Val Ala Ile Arg Glu Met Tyr Pro Lys Ala His Phe Val Thr Ile
100 105 110

ttc gca aaa ccg gct ggt cgt ccg ctg gtt gat gac tat gtt gtt gat 384
Phe Ala Lys Pro Ala Gly Arg Pro Leu Val Asp Asp Tyr Val Val Asp
115 120 125

atc ccg caa gat acc tgg att gaa cag ccg tgg gat atg ggc gtc gta 432
Ile Pro Gln Asp Thr Trp Ile Glu Gln Pro Trp Asp Met Gly Val Val
130 135 140

ttc gtc ccg cca atc tcc ggt cgc taa 459
Phe Val Pro Pro Ile Ser Gly Arg
145 150

<210> 22
<211> 152
<212> PRT
<213> Escherichia coli

<400> 22
Met Ser Glu Lys Tyr Ile Val Thr Trp Asp Met Leu Gln Ile His Ala
1 5 10 15
Arg Lys Leu Ala Ser Arg Leu Met Pro Ser Glu Gln Trp Lys Gly Ile
20 25 30
Ile Ala Val Ser Arg Gly Gly Leu Val Pro Gly Ala Leu Leu Ala Arg
35 40 45
Glu Leu Gly Ile Arg His Val Asp Thr Val Cys Ile Ser Ser Tyr Asp
50 55 60
His Asp Asn Gln Arg Glu Leu Lys Val Leu Lys Arg Ala Glu Gly Asp
65 70 75 80
Gly Glu Gly Phe Ile Val Ile Asp Asp Leu Val Asp Thr Gly Gly Thr
85 90 95
Ala Val Ala Ile Arg Glu Met Tyr Pro Lys Ala His Phe Val Thr Ile
100 105 110
Phe Ala Lys Pro Ala Gly Arg Pro Leu Val Asp Asp Tyr Val Val Asp
115 120 125
Ile Pro Gln Asp Thr Trp Ile Glu Gln Pro Trp Asp Met Gly Val Val
130 135 140
Phe Val Pro Pro Ile Ser Gly Arg
145 150

<210> 23
<211> 720
<212> DNA
<213> Escherichia coli

sequence listing

<220>

<221> CDS

<222> (1)..(717)

<223> coding for purine nucleoside phosphorylase (deoD)

<400> 23

atg gct acc cca cac att aat gca gaa atg ggc gat ttc gct gac gta	48
Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val	
1 5 10 15	
ggt ttg atg cca ggc gac ccg ctg cgt gcg aag tat att gct gaa act	96
Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr	
20 25 30	
ttc ctt gaa gat gcc cgt gaa gtg aac aac gtt cgc ggt atg ctg ggc	144
Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly	
35 40 45	
ttc acc ggt act tac aaa ggc cgc aaa att tcc gta atg ggt cac ggt	192
Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly	
50 55 60	
atg ggt atc ccg tcc tgc tcc atc tac acc aaa gaa ctg atc acc gat	240
Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp	
65 70 75 80	
ttc ggc gtg aag aaa att atc cgc gtg ggt tcc tgt ggc gca gtt ctg	288
Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu	
85 90 95	
ccg cac gta aaa ctg cgc gac gtc gtt atc ggt atg ggt gcc tgc acc	336
Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Ala Cys Thr	
100 105 110	
gat tcc aaa gtt aac cgc atc cgt ttt aaa gac cat gac ttt gcc gct	384
Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala	
115 120 125	
atc gct gac ttc gac atg gtg cgt aac gca gta gat gca gct aaa gca	432
Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala	
130 135 140	
ctg ggt att gat gct cgc gtg ggt aac ctg ttc tcc gct gac ctg ttc	480
Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe	
145 150 155 160	
tac tct ccg gac ggc gaa atg ttc gac gtg atg gaa aaa tac ggc att	528
Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile	
165 170 175	
ctc ggc gtg gaa atg gaa gcg gct ggt atc tac ggc gtc gct gca gaa	576
Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu	
180 185 190	
ttt ggc gcg aaa gcc ctg acc atc tgc acc gta tct gac cac atc cgc	624
Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg	
195 200 205	
act cac gag cag acc act gcc gct gag cgt cag act acc ttc aac gac	672
Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asp	
210 215 220	
atg atc aaa atc gca ctg gaa tcc gtt ctg ctg ggc gat aaa gag taa	720

sequence listing

Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu
225 230 235

<210> 24

<211> 239

<212> PRT

<213> Escherichia coli

<400> 24

Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val
1 5 10 15
Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr
20 25 30
Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly
35 40 45
Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly
50 55 60
Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp
65 70 75 80
Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu
85 90 95
Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Ala Cys Thr
100 105 110
Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala
115 120 125
Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala
130 135 140
Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe
145 150 155 160
Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile
165 170 175
Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu
180 185 190
Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg
195 200 205
Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asp
210 215 220
Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu
225 230 235

<210> 25

<211> 1545

<212> DNA

<213> Burkholderia caryophylli

<220>

<221> CDS

<222> (1)..(1542)

sequence listing

<223> coding for phosphonate monoester hydrolase (pehA)

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<400> 25
atg acc aga aaa aat gtc ctg ctt atc gtc gtt gat caa tgg cga gca 48
Met Thr Arg Lys Asn Val Leu Leu Ile Val Val Asp Gln Trp Arg Ala
 1          5          10          15

gat ttt atc cct cac ctg atg cgg gcg gag ggg cgc gaa cct ttc ctt 96
Asp Phe Ile Pro His Leu Met Arg Ala Glu Gly Arg Glu Pro Phe Leu
          20          25          30

aaa act ccc aat ctt gat cgt ctt tgc cgg gaa ggc ttg acc ttc cgc 144
Lys Thr Pro Asn Leu Asp Arg Leu Cys Arg Glu Gly Leu Thr Phe Arg
          35          40          45

aat cat gtc acg acg tgc gtg ccg tgt ggt ccg gca agg gca agc ctg 192
Asn His Val Thr Thr Cys Val Pro Cys Gly Pro Ala Arg Ala Ser Leu
          50          55          60

ctg acg ggc ctc tac ctg atg aac cac cgg gcg gtg cag aac act gtt 240
Leu Thr Gly Leu Tyr Leu Met Asn His Arg Ala Val Gln Asn Thr Val
          65          70          75

ccg ctt gac cag cgc cat cta aac ctt ggc aag gcc ctg cgc gcc att 288
Pro Leu Asp Gln Arg His Leu Asn Leu Gly Lys Ala Leu Arg Ala Ile
          85          90          95

ggc tac gat ccc gcg ctc att ggt tac acc acc acg aca cct gat ccg 336
Gly Tyr Asp Pro Ala Leu Ile Gly Tyr Thr Thr Thr Pro Asp Pro
          100          105          110

cgc aca acc tct gca agg gat ccg cgt ttc acg gtc ctg ggc gac atc 384
Arg Thr Thr Ser Ala Arg Asp Pro Arg Phe Thr Val Leu Gly Asp Ile
          115          120          125

atg gac ggc ttt cgt tcg gtc ggc gca ttc gag ccc aat atg gag ggg 432
Met Asp Gly Phe Arg Ser Val Gly Ala Phe Glu Pro Asn Met Glu Gly
          130          135          140

tat ttt ggc tgg gtg gcg cag aac ggc ttc gaa ctg cca gag aac cgc 480
Tyr Phe Gly Trp Val Ala Gln Asn Gly Phe Glu Leu Pro Glu Asn Arg
          145          150          155

gaa gat atc tgg ctg ccg gaa ggt gaa cat tcc gtt ccc ggt gct acc 528
Glu Asp Ile Trp Leu Pro Glu Gly Glu His Ser Val Pro Gly Ala Thr
          165          170          175

gac aaa ccg tcg cgc att ccg aag gaa ttt tcg gat tcg aca ttc ttc 576
Asp Lys Pro Ser Arg Ile Pro Lys Glu Phe Ser Asp Ser Thr Phe Phe
          180          185          190

acg gag cgc gcc ctg aca tat ctg aag ggc agg gac ggc aag cct ttc 624
Thr Glu Arg Ala Leu Thr Tyr Leu Lys Gly Arg Asp Gly Lys Pro Phe
          195          200          205

ttc ctg cat ctt ggc tat tat cgc ccg cat ccg cct ttc gta gcc tcc 672
Phe Leu His Leu Gly Tyr Tyr Arg Pro His Pro Pro Phe Val Ala Ser
          210          215          220

gcg ccc tac cat gcg atg tac aaa gcc gaa gat atg cct gcg cct ata 720
Ala Pro Tyr His Ala Met Tyr Lys Ala Glu Asp Met Pro Ala Pro Ile
          225          230          235

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sequence listing																
cgt	gcg	gag	aat	ccg	gat	gcc	gaa	gcg	gca	cag	cat	ccg	ctc	atg	aag	768
Arg	Ala	Glu	Asn	Pro	Asp	Ala	Glu	Ala	Ala	Gln	His	Pro	Leu	Met	Lys	
				245				250						255		
cac	tat	atc	gac	cac	atc	aga	cg	ggc	tcg	ttc	ttc	cat	ggc	gcg	gaa	816
His	Tyr	Ile	Asp	His	Ile	Arg	Arg	Gly	Ser	Phe	Phe	His	Gly	Ala	Glu	
			260					265					270			
ggc	tcg	gga	gca	acg	ctt	gat	gaa	ggc	gaa	att	cg	cag	atg	cg	gct	864
Gly	Ser	Gly	Ala	Thr	Leu	Asp	Glu	Gly	Glu	Ile	Arg	Gln	Met	Arg	Ala	
		275					280					285				
aca	tat	tgc	gga	ctg	atc	acc	gag	atc	gac	gat	tgt	ctg	ggg	agg	gtc	912
Thr	Tyr	Cys	Gly	Leu	Ile	Thr	Glu	Ile	Asp	Asp	Cys	Leu	Gly	Arg	Val	
	290					295					300					
ttt	gcc	tat	ctc	gat	gaa	acc	gg	cag	tgg	gac	gac	acg	ctg	att	atc	960
Phe	Ala	Tyr	Leu	Asp	Glu	Thr	Gly	Gln	Trp	Asp	Asp	Thr	Leu	Ile	Ile	
305					310					315					320	
ttc	acg	agc	gat	cat	ggc	gaa	caa	ctg	ggc	gat	cat	cac	ctg	ctc	ggc	1008
Phe	Thr	Ser	Asp	His	Gly	Glu	Gln	Leu	Gly	Asp	His	His	Leu	Leu	Gly	
				325					330					335		
aag	atc	ggt	tac	aat	gcc	gaa	agc	ttc	cg	att	ccc	ttg	gtc	ata	aag	1056
Lys	Ile	Gly	Tyr	Asn	Ala	Glu	Ser	Phe	Arg	Ile	Pro	Leu	Val	Ile	Lys	
			340					345					350			
gat	gcg	gga	cag	aac	cg	cac	gcc	ggc	cag	atc	gaa	gaa	ggc	ttc	tcc	1104
Asp	Ala	Gly	Gln	Asn	Arg	His	Ala	Gly	Gln	Ile	Glu	Glu	Gly	Phe	Ser	
		355					360					365				
gaa	agc	atc	gac	gtc	atg	ccg	acc	atc	ctc	gaa	tgg	ctg	ggc	ggg	gaa	1152
Glu	Ser	Ile	Asp	Val	Met	Pro	Thr	Ile	Leu	Glu	Trp	Leu	Gly	Gly	Glu	
	370					375					380					
acg	cct	cg	gcc	tgc	gac	ggc	cg	tcg	ctg	ttg	ccg	ttt	ctg	gct	gag	1200
Thr	Pro	Arg	Ala	Cys	Asp	Gly	Arg	Ser	Leu	Leu	Pro	Phe	Leu	Ala	Glu	
385					390					395					400	
gga	aag	ccc	tcc	gac	tgg	cg	acg	gaa	cta	cat	tac	gag	ttc	gat	ttt	1248
Gly	Lys	Pro	Ser	Asp	Trp	Arg	Thr	Glu	Leu	His	Tyr	Glu	Phe	Asp	Phe	
				405				410						415		
cg	gat	gtc	ttc	tac	gat	cag	ccg	cag	aac	tcg	gtc	cag	ctt	tcc	cag	1296
Arg	Asp	Val	Phe	Tyr	Asp	Gln	Pro	Gln	Asn	Ser	Val	Gln	Leu	Ser	Gln	
			420					425					430			
gat	gat	tgc	agc	ctc	tgt	gtg	atc	gag	gac	gaa	aac	tac	aag	tac	gtg	1344
Asp	Asp	Cys	Ser	Leu	Cys	Val	Ile	Glu	Asp	Glu	Asn	Tyr	Lys	Tyr	Val	
		435					440					445				
cat	ttt	gcc	gcc	ctg	ccg	ccg	ctg	ttc	ttc	gat	ctg	aag	gca	gac	ccg	1392
His	Phe	Ala	Ala	Leu	Pro	Pro	Leu	Phe	Phe	Asp	Leu	Lys	Ala	Asp	Pro	
	450					455					460					
cat	gaa	ttc	agc	aat	ctg	gct	ggc	gat	cct	gct	tat	gcg	gcc	ctc	gtt	1440
His	Glu	Phe	Ser	Asn	Leu	Ala	Gly	Asp	Pro	Ala	Tyr	Ala	Ala	Leu	Val	
465					470					475					480	
cg	gac	tat	gcc	cag	aag	gca	ttg	tcg	tgg	cga	ctg	tct	cat	gcc	gac	1488
Arg	Asp	Tyr	Ala	Gln	Lys	Ala	Leu	Ser	Trp	Arg	Leu	Ser	His	Ala	Asp	
				485					490					495		

sequence listing

cgg aca ctc acc cat tac aga tcc agc ccg caa ggg ctg aca acg cgc 1536
 Arg Thr Leu Thr His Tyr Arg Ser Ser Pro Gln Gly Leu Thr Thr Arg
 500 505 510

aac cat tga 1545
 Asn His

<210> 26
 <211> 514
 <212> PRT
 <213> Burkholderia caryophylli

<400> 26
 Met Thr Arg Lys Asn Val Leu Leu Ile Val Val Asp Gln Trp Arg Ala
 1 5 10 15
 Asp Phe Ile Pro His Leu Met Arg Ala Glu Gly Arg Glu Pro Phe Leu
 20 25 30
 Lys Thr Pro Asn Leu Asp Arg Leu Cys Arg Glu Gly Leu Thr Phe Arg
 35 40 45
 Asn His Val Thr Thr Cys Val Pro Cys Gly Pro Ala Arg Ala Ser Leu
 50 55 60
 Leu Thr Gly Leu Tyr Leu Met Asn His Arg Ala Val Gln Asn Thr Val
 65 70 75 80
 Pro Leu Asp Gln Arg His Leu Asn Leu Gly Lys Ala Leu Arg Ala Ile
 85 90 95
 Gly Tyr Asp Pro Ala Leu Ile Gly Tyr Thr Thr Thr Thr Pro Asp Pro
 100 105 110
 Arg Thr Thr Ser Ala Arg Asp Pro Arg Phe Thr Val Leu Gly Asp Ile
 115 120 125
 Met Asp Gly Phe Arg Ser Val Gly Ala Phe Glu Pro Asn Met Glu Gly
 130 135 140
 Tyr Phe Gly Trp Val Ala Gln Asn Gly Phe Glu Leu Pro Glu Asn Arg
 145 150 155 160
 Glu Asp Ile Trp Leu Pro Glu Gly Glu His Ser Val Pro Gly Ala Thr
 165 170 175
 Asp Lys Pro Ser Arg Ile Pro Lys Glu Phe Ser Asp Ser Thr Phe Phe
 180 185 190
 Thr Glu Arg Ala Leu Thr Tyr Leu Lys Gly Arg Asp Gly Lys Pro Phe
 195 200 205
 Phe Leu His Leu Gly Tyr Tyr Arg Pro His Pro Pro Phe Val Ala Ser
 210 215 220
 Ala Pro Tyr His Ala Met Tyr Lys Ala Glu Asp Met Pro Ala Pro Ile
 225 230 235 240
 Arg Ala Glu Asn Pro Asp Ala Glu Ala Ala Gln His Pro Leu Met Lys
 245 250 255
 His Tyr Ile Asp His Ile Arg Arg Gly Ser Phe Phe His Gly Ala Glu

sequence listing

260 265 270

Gly Ser Gly Ala Thr Leu Asp Glu Gly Glu Ile Arg Gln Met Arg Ala
275 280 285

Thr Tyr Cys Gly Leu Ile Thr Glu Ile Asp Asp Cys Leu Gly Arg Val
290 295 300

Phe Ala Tyr Leu Asp Glu Thr Gly Gln Trp Asp Asp Thr Leu Ile Ile
305 310 315 320

Phe Thr Ser Asp His Gly Glu Gln Leu Gly Asp His His Leu Leu Gly
325 330 335

Lys Ile Gly Tyr Asn Ala Glu Ser Phe Arg Ile Pro Leu Val Ile Lys
340 345 350

Asp Ala Gly Gln Asn Arg His Ala Gly Gln Ile Glu Glu Gly Phe Ser
355 360 365

Glu Ser Ile Asp Val Met Pro Thr Ile Leu Glu Trp Leu Gly Gly Glu
370 375 380

Thr Pro Arg Ala Cys Asp Gly Arg Ser Leu Leu Pro Phe Leu Ala Glu
385 390 395 400

Gly Lys Pro Ser Asp Trp Arg Thr Glu Leu His Tyr Glu Phe Asp Phe
405 410 415

Arg Asp Val Phe Tyr Asp Gln Pro Gln Asn Ser Val Gln Leu Ser Gln
420 425 430

Asp Asp Cys Ser Leu Cys Val Ile Glu Asp Glu Asn Tyr Lys Tyr Val
435 440 445

His Phe Ala Ala Leu Pro Pro Leu Phe Phe Asp Leu Lys Ala Asp Pro
450 455 460

His Glu Phe Ser Asn Leu Ala Gly Asp Pro Ala Tyr Ala Ala Leu Val
465 470 475 480

Arg Asp Tyr Ala Gln Lys Ala Leu Ser Trp Arg Leu Ser His Ala Asp
485 490 495

Arg Thr Leu Thr His Tyr Arg Ser Ser Pro Gln Gly Leu Thr Thr Arg
500 505 510

Asn His

<210> 27
<211> 2250
<212> DNA
<213> Agrobacterium rhizogenes
<220>
<221> CDS
<222> (1)..(2247)
<223> coding for tryptophan oxygenase (aux1)

<400> 27
atg gct gga tcc tcc ttc aca ttg cca tca act ggc tca gcg ccc ctt 48
Met Ala Gly Ser Ser Phe Thr Leu Pro Ser Thr Gly Ser Ala Pro Leu
1 5 10 15

sequence listing

gat atg atg ctt atc gat gat tca gat ctg ctg caa ttg ggt ctc cag	96
Asp Met Met Leu Ile Asp Asp Ser Asp Leu Leu Gln Leu Gly Leu Gln	
20 25 30	
cag gta ttc tcg aag cgg tac aca gag aca ccg cag tca cgc tac aaa	144
Gln Val Phe Ser Lys Arg Tyr Thr Glu Thr Pro Gln Ser Arg Tyr Lys	
35 40 45	
ctg acc agg agg gct tct cca gac gtc tca tct ggc gaa ggc aat gtg	192
Leu Thr Arg Arg Ala Ser Pro Asp Val Ser Ser Gly Glu Gly Asn Val	
50 55 60	
cat gcc ctt gcg ttc ata tat gtc aac gct gag acg ttg cag atg atc	240
His Ala Leu Ala Phe Ile Tyr Val Asn Ala Glu Thr Leu Gln Met Ile	
65 70 75 80	
aaa aac gct cga tcg cta acc gaa gcg aac ggc gtc aaa gat ctt gtc	288
Lys Asn Ala Arg Ser Leu Thr Glu Ala Asn Gly Val Lys Asp Leu Val	
85 90 95	
gcc atc gac gtt ccg cca ttt cga aac gac ttc tca aga gcg cta ctc	336
Ala Ile Asp Val Pro Pro Phe Arg Asn Asp Phe Ser Arg Ala Leu Leu	
100 105 110	
ctt caa gtg atc aac ttg ttg gga aac aac cga aat gcc gat gac gat	384
Leu Gln Val Ile Asn Leu Leu Gly Asn Asn Arg Asn Ala Asp Asp Asp	
115 120 125	
ctt agt cac ttc ata gca gtt gct ctc cca aac agc gcc cgc tct aag	432
Leu Ser His Phe Ile Ala Val Ala Leu Pro Asn Ser Ala Arg Ser Lys	
130 135 140	
atc cta acc acg gca ccg ttc gaa gga agc ttg tca gaa aac ttc agg	480
Ile Leu Thr Thr Ala Pro Phe Glu Gly Ser Leu Ser Glu Asn Phe Arg	
145 150 155 160	
ggg ttc ccg atc act cgt gaa gga aat gtg gca tgt gaa gtg cta gcc	528
Gly Phe Pro Ile Thr Arg Glu Gly Asn Val Ala Cys Glu Val Leu Ala	
165 170 175	
tat ggg aat aac ttg atg ccc aag gcc tgc tcc gat tcc ttt cca acc	576
Tyr Gly Asn Asn Leu Met Pro Lys Ala Cys Ser Asp Ser Phe Pro Thr	
180 185 190	
gtg gat ctt ctt tat gac tat ggc aag ttc ttc gag agt tgc gcg gcc	624
Val Asp Leu Leu Tyr Asp Tyr Gly Lys Phe Phe Glu Ser Cys Ala Ala	
195 200 205	
gat gga cgt atc ggt tat ttt cct gaa ggc gtt acg aaa cct aaa gtg	672
Asp Gly Arg Ile Gly Tyr Phe Pro Glu Gly Val Thr Lys Pro Lys Val	
210 215 220	
gct ata att ggc gca ggc ttt tcc ggg ctc gtt gca gcg agc gaa cta	720
Ala Ile Ile Gly Ala Gly Phe Ser Gly Leu Val Ala Ala Ser Glu Leu	
225 230 235 240	
ctt cat gca ggg gta gac gat gtt acg gtg tat gag gcg agt gat cgg	768
Leu His Ala Gly Val Asp Asp Val Thr Val Tyr Glu Ala Ser Asp Arg	
245 250 255	
ctt gga gga aag cta tgg tca cac gga ttt aag agt gct cca aat gtg	816
Leu Gly Gly Lys Leu Trp Ser His Gly Phe Lys Ser Ala Pro Asn Val	

sequence listing																
260					265					270						
ata	gcc	gag	atg	ggg	gcc	atg	cgt	ttt	ccg	cga	agt	gaa	tca	tgc	ttg	864
Ile	Ala	Glu	Met	Gly	Ala	Met	Arg	Phe	Pro	Arg	Ser	Glu	Ser	Cys	Leu	
		275					280					285				
ttc	ttc	tat	ctc	aaa	aag	cac	gga	ctg	gac	tcc	gtt	ggt	ctg	ttc	ccg	912
Phe	Phe	Tyr	Leu	Lys	Lys	His	Gly	Leu	Asp	Ser	Val	Gly	Leu	Phe	Pro	
		290				295					300					
aat	ccg	gga	agt	gtc	gat	acc	gca	ttg	ttc	tac	agg	ggc	cgt	caa	tat	960
Asn	Pro	Gly	Ser	Val	Asp	Thr	Ala	Leu	Phe	Tyr	Arg	Gly	Arg	Gln	Tyr	
		305			310					315					320	
atc	tgg	aaa	gcg	gga	gag	gag	cca	ccg	gag	ctg	ttt	cgt	cgt	gtg	cac	1008
Ile	Trp	Lys	Ala	Gly	Glu	Glu	Pro	Pro	Glu	Leu	Phe	Arg	Arg	Val	His	
				325					330					335		
cat	gga	tgg	cgc	gca	ttt	ttg	caa	gat	ggc	tat	ctc	cat	gat	gga	gtc	1056
His	Gly	Trp	Arg	Ala	Phe	Leu	Gln	Asp	Gly	Tyr	Leu	His	Asp	Gly	Val	
			340					345					350			
atg	ttg	gcg	tca	ccg	tta	gca	att	gtt	gac	gcc	ttg	aat	tta	ggg	cat	1104
Met	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Val	Asp	Ala	Leu	Asn	Leu	Gly	His	
		355					360					365				
cta	cag	cag	gcg	cat	ggc	ttc	tgg	caa	tct	tgg	ctc	aca	tat	ttt	gag	1152
Leu	Gln	Gln	Ala	His	Gly	Phe	Trp	Gln	Ser	Trp	Leu	Thr	Tyr	Phe	Glu	
		370				375					380					
cga	gag	tct	ttc	tct	tct	ggc	atc	gaa	aaa	atg	ttc	ttg	ggc	aat	cat	1200
Arg	Glu	Ser	Phe	Ser	Ser	Gly	Ile	Glu	Lys	Met	Phe	Leu	Gly	Asn	His	
					390					395					400	
cct	ccg	ggg	ggt	gaa	caa	tgg	aat	tcc	cta	gat	gac	ttg	gat	ctt	ttc	1248
Pro	Pro	Gly	Gly	Glu	Gln	Trp	Asn	Ser	Leu	Asp	Asp	Leu	Asp	Leu	Phe	
				405					410					415		
aaa	gcg	ctg	ggt	att	gga	tcc	ggc	gga	ttc	ggc	cct	gta	ttt	gaa	agt	1296
Lys	Ala	Leu	Gly	Ile	Gly	Ser	Gly	Gly	Phe	Gly	Pro	Val	Phe	Glu	Ser	
			420					425					430			
ggg	ttt	atc	gag	atc	ctt	cgc	tta	gtc	gtc	aac	ggg	tat	gag	gat	aac	1344
Gly	Phe	Ile	Glu	Ile	Leu	Arg	Leu	Val	Val	Asn	Gly	Tyr	Glu	Asp	Asn	
		435					440					445				
gtg	cgg	ctg	agt	tac	gaa	gga	att	tct	gag	ctg	cct	cat	agg	atc	gcc	1392
Val	Arg	Leu	Ser	Tyr	Glu	Gly	Ile	Ser	Glu	Leu	Pro	His	Arg	Ile	Ala	
		450				455					460					
tca	cag	gta	att	aac	ggc	aga	tct	att	cgc	gag	cgt	aca	att	cac	gtt	1440
Ser	Gln	Val	Ile	Asn	Gly	Arg	Ser	Ile	Arg	Glu	Arg	Thr	Ile	His	Val	
					470					475					480	
caa	gtc	gag	cag	att	gat	aga	gag	gag	gat	aaa	ata	aat	atc	aag	atc	1488
Gln	Val	Glu	Gln	Ile	Asp	Arg	Glu	Glu	Asp	Lys	Ile	Asn	Ile	Lys	Ile	
				485					490					495		
aaa	gga	gga	aag	gtt	gag	gtc	tat	gat	cga	gta	ctg	gtt	aca	tcc	ggg	1536
Lys	Gly	Gly	Lys	Val	Glu	Val	Tyr	Asp	Arg	Val	Leu	Val	Thr	Ser	Gly	
			500					505					510			
ttt	gcg	aac	atc	gaa	atg	cgc	cat	ctc	ctg	aca	tca	agc	aac	gca	ttc	1584

sequence listing																
Phe	Ala	Asn	Ile	Glu	Met	Arg	His	Leu	Leu	Thr	Ser	Ser	Asn	Ala	Phe	
		515					520					525				
ttc	cat	gca	gat	gta	agc	cat	gca	ata	ggg	aac	agt	cat	atg	act	ggt	1632
Phe	His	Ala	Asp	Val	Ser	His	Ala	Ile	Gly	Asn	Ser	His	Met	Thr	Gly	
		530				535					540					
gcg	tca	aaa	ctg	ttc	ttg	ctg	act	aac	gaa	aaa	ttc	tgg	cta	caa	cat	1680
Ala	Ser	Lys	Leu	Phe	Leu	Leu	Thr	Asn	Glu	Lys	Phe	Trp	Leu	Gln	His	
		545			550					555					560	
cat	ttg	cca	tcg	tgc	ata	ctc	acc	acc	ggc	gtt	gca	aag	gca	gtt	tat	1728
His	Leu	Pro	Ser	Cys	Ile	Leu	Thr	Thr	Gly	Val	Ala	Lys	Ala	Val	Tyr	
				565					570					575		
tgc	tta	gac	tat	gat	ccg	cga	gat	cca	agc	ggc	aaa	gga	ctg	gtg	ttg	1776
Cys	Leu	Asp	Tyr	Asp	Pro	Arg	Asp	Pro	Ser	Gly	Lys	Gly	Leu	Val	Leu	
			580					585					590			
ata	agc	tat	act	tgg	gag	gat	gac	tca	cat	aag	ctc	cta	gcc	gtc	ccc	1824
Ile	Ser	Tyr	Thr	Trp	Glu	Asp	Asp	Ser	His	Lys	Leu	Leu	Ala	Val	Pro	
		595					600					605				
gac	aaa	aga	gaa	agg	ttc	gca	tcg	ctg	cag	cgc	gat	att	ggg	agg	gca	1872
Asp	Lys	Arg	Glu	Arg	Phe	Ala	Ser	Leu	Gln	Arg	Asp	Ile	Gly	Arg	Ala	
		610				615					620					
ttc	cca	gat	ttt	gcc	aag	cac	cta	act	cct	gca	gac	ggg	aac	tat	gat	1920
Phe	Pro	Asp	Phe	Ala	Lys	His	Leu	Thr	Pro	Ala	Asp	Gly	Asn	Tyr	Asp	
		625			630					635					640	
gat	aat	atc	gtt	caa	cat	gat	tgg	ctg	act	gat	ccc	cac	gct	ggc	gga	1968
Asp	Asn	Ile	Val	Gln	His	Asp	Trp	Leu	Thr	Asp	Pro	His	Ala	Gly	Gly	
				645					650					655		
gcg	ttt	aaa	ctg	aac	cgc	aga	ggc	aac	gac	gta	tat	tca	gaa	agg	ctt	2016
Ala	Phe	Lys	Leu	Asn	Arg	Arg	Gly	Asn	Asp	Val	Tyr	Ser	Glu	Arg	Leu	
			660					665					670			
ttc	ttt	cag	ccc	ttt	gac	gta	atg	cat	ccc	gcg	gac	gat	aag	gga	ctt	2064
Phe	Phe	Gln	Pro	Phe	Asp	Val	Met	His	Pro	Ala	Asp	Asp	Lys	Gly	Leu	
		675				680						685				
tac	ttg	gcc	ggg	tgt	agc	tgt	tcc	ttc	acc	gga	ggg	tgg	gtt	cat	ggg	2112
Tyr	Leu	Ala	Gly	Cys	Ser	Cys	Ser	Phe	Thr	Gly	Gly	Trp	Val	His	Gly	
		690				695					700					
gcc	att	cag	acc	gca	tgc	aac	gct	acg	tgt	gcg	atc	att	tat	ggg	tcc	2160
Ala	Ile	Gln	Thr	Ala	Cys	Asn	Ala	Thr	Cys	Ala	Ile	Ile	Tyr	Gly	Ser	
				710						715					720	
gga	cac	ctg	caa	gag	cta	atc	cac	tgg	cga	cac	ctc	aaa	gaa	ggg	aat	2208
Gly	His	Leu	Gln	Glu	Leu	Ile	His	Trp	Arg	His	Leu	Lys	Glu	Gly	Asn	
				725					730					735		
cca	ctg	gcg	cac	gct	tgg	aag	cgg	tat	agg	tat	caa	gcg	tga			2250
Pro	Leu	Ala	His	Ala	Trp	Lys	Arg	Tyr	Arg	Tyr	Gln	Ala				
			740					745								

<210> 28
 <211> 749
 <212> PRT

sequence listing

<213> Agrobacterium rhizogenes

<400> 28

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Met Ala Gly Ser Ser Phe Thr Leu Pro Ser Thr Gly Ser Ala Pro Leu
 1          5          10          15

Asp Met Met Leu Ile Asp Asp Ser Asp Leu Leu Gln Leu Gly Leu Gln
 20          25          30

Gln Val Phe Ser Lys Arg Tyr Thr Glu Thr Pro Gln Ser Arg Tyr Lys
 35          40          45

Leu Thr Arg Arg Ala Ser Pro Asp Val Ser Ser Gly Glu Gly Asn Val
 50          55          60

His Ala Leu Ala Phe Ile Tyr Val Asn Ala Glu Thr Leu Gln Met Ile
 65          70          75          80

Lys Asn Ala Arg Ser Leu Thr Glu Ala Asn Gly Val Lys Asp Leu Val
 85          90          95

Ala Ile Asp Val Pro Pro Phe Arg Asn Asp Phe Ser Arg Ala Leu Leu
100          105          110

Leu Gln Val Ile Asn Leu Leu Gly Asn Asn Arg Asn Ala Asp Asp Asp
115          120          125

Leu Ser His Phe Ile Ala Val Ala Leu Pro Asn Ser Ala Arg Ser Lys
130          135          140

Ile Leu Thr Thr Ala Pro Phe Glu Gly Ser Leu Ser Glu Asn Phe Arg
145          150          155          160

Gly Phe Pro Ile Thr Arg Glu Gly Asn Val Ala Cys Glu Val Leu Ala
165          170          175

Tyr Gly Asn Asn Leu Met Pro Lys Ala Cys Ser Asp Ser Phe Pro Thr
180          185          190

Val Asp Leu Leu Tyr Asp Tyr Gly Lys Phe Phe Glu Ser Cys Ala Ala
195          200          205

Asp Gly Arg Ile Gly Tyr Phe Pro Glu Gly Val Thr Lys Pro Lys Val
210          215          220

Ala Ile Ile Gly Ala Gly Phe Ser Gly Leu Val Ala Ala Ser Glu Leu
225          230          235          240

Leu His Ala Gly Val Asp Asp Val Thr Val Tyr Glu Ala Ser Asp Arg
245          250          255

Leu Gly Gly Lys Leu Trp Ser His Gly Phe Lys Ser Ala Pro Asn Val
260          265          270

Ile Ala Glu Met Gly Ala Met Arg Phe Pro Arg Ser Glu Ser Cys Leu
275          280          285

Phe Phe Tyr Leu Lys Lys His Gly Leu Asp Ser Val Gly Leu Phe Pro
290          295          300

Asn Pro Gly Ser Val Asp Thr Ala Leu Phe Tyr Arg Gly Arg Gln Tyr
305          310          315          320

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sequence listing

Ile Trp Lys Ala Gly Glu Glu Pro Pro Glu Leu Phe Arg Arg Val His
325 330 335

His Gly Trp Arg Ala Phe Leu Gln Asp Gly Tyr Leu His Asp Gly Val
340 345 350

Met Leu Ala Ser Pro Leu Ala Ile Val Asp Ala Leu Asn Leu Gly His
355 360 365

Leu Gln Gln Ala His Gly Phe Trp Gln Ser Trp Leu Thr Tyr Phe Glu
370 375 380

Arg Glu Ser Phe Ser Ser Gly Ile Glu Lys Met Phe Leu Gly Asn His
385 390 395 400

Pro Pro Gly Gly Glu Gln Trp Asn Ser Leu Asp Asp Leu Asp Leu Phe
405 410 415

Lys Ala Leu Gly Ile Gly Ser Gly Gly Phe Gly Pro Val Phe Glu Ser
420 425 430

Gly Phe Ile Glu Ile Leu Arg Leu Val Val Asn Gly Tyr Glu Asp Asn
435 440 445

Val Arg Leu Ser Tyr Glu Gly Ile Ser Glu Leu Pro His Arg Ile Ala
450 455 460

Ser Gln Val Ile Asn Gly Arg Ser Ile Arg Glu Arg Thr Ile His Val
465 470 475 480

Gln Val Glu Gln Ile Asp Arg Glu Glu Asp Lys Ile Asn Ile Lys Ile
485 490 495

Lys Gly Gly Lys Val Glu Val Tyr Asp Arg Val Leu Val Thr Ser Gly
500 505 510

Phe Ala Asn Ile Glu Met Arg His Leu Leu Thr Ser Ser Asn Ala Phe
515 520 525

Phe His Ala Asp Val Ser His Ala Ile Gly Asn Ser His Met Thr Gly
530 535 540

Ala Ser Lys Leu Phe Leu Leu Thr Asn Glu Lys Phe Trp Leu Gln His
545 550 555 560

His Leu Pro Ser Cys Ile Leu Thr Thr Gly Val Ala Lys Ala Val Tyr
565 570 575

Cys Leu Asp Tyr Asp Pro Arg Asp Pro Ser Gly Lys Gly Leu Val Leu
580 585 590

Ile Ser Tyr Thr Trp Glu Asp Asp Ser His Lys Leu Leu Ala Val Pro
595 600 605

Asp Lys Arg Glu Arg Phe Ala Ser Leu Gln Arg Asp Ile Gly Arg Ala
610 615 620

Phe Pro Asp Phe Ala Lys His Leu Thr Pro Ala Asp Gly Asn Tyr Asp
625 630 635 640

Asp Asn Ile Val Gln His Asp Trp Leu Thr Asp Pro His Ala Gly Gly
645 650 655

sequence listing

Ala Phe Lys Leu Asn Arg Arg Gly Asn Asp Val Tyr Ser Glu Arg Leu
660 665 670
Phe Phe Gln Pro Phe Asp Val Met His Pro Ala Asp Asp Lys Gly Leu
675 680 685
Tyr Leu Ala Gly Cys Ser Cys Ser Phe Thr Gly Gly Trp Val His Gly
690 695 700
Ala Ile Gln Thr Ala Cys Asn Ala Thr Cys Ala Ile Ile Tyr Gly Ser
705 710 715 720
Gly His Leu Gln Glu Leu Ile His Trp Arg His Leu Lys Glu Gly Asn
725 730 735
Pro Leu Ala His Ala Trp Lys Arg Tyr Arg Tyr Gln Ala
740 745

<210> 29
<211> 1401
<212> DNA
<213> Agrobacterium rhizogenes
<220>
<221> CDS
<222> (1)..(1398)
<223> coding for indoleacetamide hydrolase

<400> 29
atg gtg acc ctc tcc tcg atc acc gag acg ctt aaa tgt ctc agg gaa 48
Met Val Thr Leu Ser Ser Ile Thr Glu Thr Leu Lys Cys Leu Arg Glu
1 5 10 15
aga aaa tac tcg tgc ttt gag tta atc gaa acg ata ata gcc cgc tgt 96
Arg Lys Tyr Ser Cys Phe Glu Leu Ile Glu Thr Ile Ile Ala Arg Cys
20 25 30
gaa gca gca aga tcc tta aac gcc ttt ctg gaa acc gac tgg gcg cac 144
Glu Ala Ala Arg Ser Leu Asn Ala Phe Leu Glu Thr Asp Trp Ala His
35 40 45
cta cgg tgg act gcc agc aaa atc gat caa cac gga ggt gcc ggt gtt 192
Leu Arg Trp Thr Ala Ser Lys Ile Asp Gln His Gly Gly Ala Gly Val
50 55 60
ggc cta gct ggc gtt ccc cta tgc ttt aaa gcg aat att gcg aca ggc 240
Gly Leu Ala Gly Val Pro Leu Cys Phe Lys Ala Asn Ile Ala Thr Gly
65 70 75 80
agg ttc gcc gcg acc gct ggt acg cca ggc tta cag aac cac aaa ccc 288
Arg Phe Ala Ala Thr Ala Gly Thr Pro Gly Leu Gln Asn His Lys Pro
85 90 95
aag acg cct gcc gga gtt gca cga caa ctt ctc gcg gct ggg gca ctg 336
Lys Thr Pro Ala Gly Val Ala Arg Gln Leu Leu Ala Ala Gly Ala Leu
100 105 110
cct ggc gct tcg gga aac atg cac gaa ttg tct ttt ggg atc acg agc 384
Pro Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser
115 120 125
aac aac ttc gcc aca ggc gcc gta cga aac ccg tgg aac cct agt ctc 432
Asn Asn Phe Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu
130 135 140

sequence listing

atc cca ggg gga tca agt ggg ggt gtg gcc gcc gcg gtg gcc ggc cga Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Ala Val Ala Gly Arg 145 150 155 160	480
ttg atg ctg ggc ggc gtc gga act gac acg gga gcg tcg gtc cgt tta Leu Met Leu Gly Gly Val Gly Thr Asp Thr Gly Ala Ser Val Arg Leu 165 170 175	528
ccg gcc gcc ttg tgc ggc gtg gtg ggg ttt cgt cct acc gtg ggg cga Pro Ala Ala Leu Cys Gly Val Val Gly Phe Arg Pro Thr Val Gly Arg 180 185 190	576
tat cca acg gac gga ata gtt ccg gta agc ccc acc cgg gac acc cct Tyr Pro Thr Asp Gly Ile Val Pro Val Ser Pro Thr Arg Asp Thr Pro 195 200 205	624
ggc gtt atc gca cag aat gtt ccg gac gtg att ctt ctt gac ggt atc Gly Val Ile Ala Gln Asn Val Pro Asp Val Ile Leu Leu Asp Gly Ile 210 215 220	672
att tgc ggg aga ccg ccg gtt aat caa acg gtc cgc ctg aag ggg ctg Ile Cys Gly Arg Pro Pro Val Asn Gln Thr Val Arg Leu Lys Gly Leu 225 230 235 240	720
cgt ata ggc ttg cca acc gct tac ttt tac aac gac ctg gag ccc gat Arg Ile Gly Leu Pro Thr Ala Tyr Phe Tyr Asn Asp Leu Glu Pro Asp 245 250 255	768
gtc gcc tta gca gcc gag acg att atc aga gtt ctg gca cgc aaa gat Val Ala Leu Ala Ala Glu Thr Ile Ile Arg Val Leu Ala Arg Lys Asp 260 265 270	816
gtt act ttt gtt gaa gca gat att cct gat tta gcg cat cac aat gaa Val Thr Phe Val Glu Ala Asp Ile Pro Asp Leu Ala His His Asn Glu 275 280 285	864
ggg gtc agc ttt ccg act gcc atc tac gaa ttt ccg ttg tcc ctt gaa Gly Val Ser Phe Pro Thr Ala Ile Tyr Glu Phe Pro Leu Ser Leu Glu 290 295 300	912
cat tat att cag aac ttc gta gag ggt gtt tcc ttt tct gag gtt gtc His Tyr Ile Gln Asn Phe Val Glu Gly Val Ser Phe Ser Glu Val Val 305 310 315 320	960
aga gcg att cgc agt ccg gat gtt gca agt att ctc aat gca caa ctc Arg Ala Ile Arg Ser Pro Asp Val Ala Ser Ile Leu Asn Ala Gln Leu 325 330 335	1008
tcg gat aat ctt att tcc aaa agc gag tat tgt ctg gcg cga cgt ttt Ser Asp Asn Leu Ile Ser Lys Ser Glu Tyr Cys Leu Ala Arg Arg Phe 340 345 350	1056
ttc aga ccg aga ctc caa gcg gcc tac cac agt tac ttc aag gcg cat Phe Arg Pro Arg Leu Gln Ala Ala Tyr His Ser Tyr Phe Lys Ala His 355 360 365	1104
cag cta gat gca att ctt ttc cca aca gct ccg ttg aca gcc aag cca Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Thr Ala Lys Pro 370 375 380	1152
att ggc cat gat cta tcg gtg att cac aat ggc tca atg acc gat acc Ile Gly His Asp Leu Ser Val Ile His Asn Gly Ser Met Thr Asp Thr 1200	

385	sequence listing																400
390	395																400
ttt aaa atc ttc gtg cgg aat gta gat ccc agc agt aat gcg ggc ctg																	1248
Phe Lys Ile Phe Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu																	
	405 410 415																
ccg ggc cta agt ctt ccc gtt tct ctt agt tcc aac ggt ctg cct att																	1296
Pro Gly Leu Ser Leu Pro Val Ser Leu Ser Ser Asn Gly Leu Pro Ile																	
	420 425 430																
ggc atg gaa atc gat ggc tct gca agc tcg gat gaa cgt ctg tta gca																	1344
Gly Met Glu Ile Asp Gly Ser Ala Ser Ser Asp Glu Arg Leu Leu Ala																	
	435 440 445																
att gga cta gcg ata gaa gaa gca ata gac ttt agg cat cgt ccg act																	1392
Ile Gly Leu Ala Ile Glu Glu Ala Ile Asp Phe Arg His Arg Pro Thr																	
	450 455 460																
ctg tcg taa																	1401
Leu Ser																	
465																	

<210> 30
 <211> 466
 <212> PRT
 <213> Agrobacterium rhizogenes

<400> 30
 Met Val Thr Leu Ser Ser Ile Thr Glu Thr Leu Lys Cys Leu Arg Glu
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 Arg Lys Tyr Ser Cys Phe Glu Leu Ile Glu Thr Ile Ile Ala Arg Cys
 20 25 30
 Glu Ala Ala Arg Ser Leu Asn Ala Phe Leu Glu Thr Asp Trp Ala His
 35 40 45
 Leu Arg Trp Thr Ala Ser Lys Ile Asp Gln His Gly Gly Ala Gly Val
 50 55 60
 Gly Leu Ala Gly Val Pro Leu Cys Phe Lys Ala Asn Ile Ala Thr Gly
 65 70 75 80
 Arg Phe Ala Ala Thr Ala Gly Thr Pro Gly Leu Gln Asn His Lys Pro
 85 90 95
 Lys Thr Pro Ala Gly Val Ala Arg Gln Leu Leu Ala Ala Gly Ala Leu
 100 105 110
 Pro Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser
 115 120 125
 Asn Asn Phe Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu
 130 135 140
 Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Val Ala Gly Arg
 145 150 155 160
 Leu Met Leu Gly Gly Val Gly Thr Asp Thr Gly Ala Ser Val Arg Leu
 165 170 175
 Pro Ala Ala Leu Cys Gly Val Val Gly Phe Arg Pro Thr Val Gly Arg

sequence listing

180	185	190
Tyr Pro Thr Asp Gly Ile Val 195	Pro Val Ser Pro Thr Arg 200	Asp Thr Pro 205
Gly Val Ile Ala Gln Asn Val 210	Pro Asp Val Ile Leu 215	Leu Asp Gly Ile 220
Ile Cys Gly Arg Pro Pro Val 225	Asn Gln Thr Val Arg 230	Leu Lys Gly Leu 235
Arg Ile Gly Leu Pro Thr Ala Tyr Phe 245	Tyr Asn Asp Leu Glu Pro 250	Asp 255
Val Ala Leu Ala Ala Glu Thr Ile Ile 260	Arg Val Leu Ala Arg 265	Lys Asp 270
Val Thr Phe Val Glu Ala Asp Ile 275	Pro Asp Leu Ala His 280	His Asn Glu 285
Gly Val Ser Phe Pro Thr Ala Ile Tyr Glu Phe 290	Pro Leu Ser Leu Glu 295	
His Tyr Ile Gln Asn Phe Val Glu Gly Val 305	Ser Phe Ser Glu Val Val 310	
Arg Ala Ile Arg Ser Pro Asp Val Ala Ser 325	Ile Leu Asn Ala Gln Leu 330	
Ser Asp Asn Leu Ile Ser Lys Ser Glu Tyr Cys Leu Ala 340	Arg Arg Phe 345	
Phe Arg Pro Arg Leu Gln Ala Ala Tyr His Ser Tyr Phe 355	Lys Ala His 360	
Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Thr Ala Lys Pro 370		
Ile Gly His Asp Leu Ser Val Ile His Asn Gly Ser Met Thr Asp Thr 385		
Phe Lys Ile Phe Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu 405		
Pro Gly Leu Ser Leu Pro Val Ser Leu Ser Ser Asn Gly Leu Pro Ile 420		
Gly Met Glu Ile Asp Gly Ser Ala Ser Ser Asp Glu Arg Leu Leu Ala 435		
Ile Gly Leu Ala Ile Glu Glu Ala Ile Asp Phe Arg His Arg Pro Thr 450		
Leu Ser 465		

<210> 31
 <211> 2268
 <212> DNA
 <213> Agrobacterium tumefaciens
 <220>
 <221> CDS

sequence listing

<222> (1)..(2265)

<223> coding for tryptophan monooxygenase

<400> 31

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aaa atg gtg gat ctg ata atg gtc gat aag gct gat gaa ttg gac cgc	96
Lys Met Val Asp Leu Ile Met Val Asp Lys Ala Asp Glu Leu Asp Arg	
20 25 30	
agg gtt tcc gat gcc ttc tca gaa cgt gaa gct tct agg gga agg agg	144
Arg Val Ser Asp Ala Phe Ser Glu Arg Glu Ala Ser Arg Gly Arg Arg	
35 40 45	
att act caa atc tcc ggc gag tgc agc gct ggg tta gct tgc aaa agg	192
Ile Thr Gln Ile Ser Gly Glu Cys Ser Ala Gly Leu Ala Cys Lys Arg	
50 55 60	
ctg gcc gac ggt cgc ttt ccc gag atc tca act ggt gag aag gta gca	240
Leu Ala Asp Gly Arg Phe Pro Glu Ile Ser Thr Gly Glu Lys Val Ala	
65 70 75 80	
gcc ctc tcc gct tac atc tat gtt ggc aag gaa att ctg ggg cgg ata	288
Ala Leu Ser Ala Tyr Ile Tyr Val Gly Lys Glu Ile Leu Gly Arg Ile	
85 90 95	
ctt gaa tcg gaa cct tgg gcg cga gca aga gtg agt ggt ctc gtt gcc	336
Leu Glu Ser Glu Pro Trp Ala Arg Ala Arg Val Ser Gly Leu Val Ala	
100 105 110	
atc gac ctt gca cca ttt tgt atg gat ttc tcc gaa gca caa ctt ctc	384
Ile Asp Leu Ala Pro Phe Cys Met Asp Phe Ser Glu Ala Gln Leu Leu	
115 120 125	
caa acc ctg ttt ttg ctg agc ggt aaa aga tgt gca tcc agc gat ctt	432
Gln Thr Leu Phe Leu Leu Ser Gly Lys Arg Cys Ala Ser Ser Asp Leu	
130 135 140	
agt cat ttc gtg gcc att tca atc tct aag act gcc cgc tcc cga acc	480
Ser His Phe Val Ala Ile Ser Ile Ser Lys Thr Ala Arg Ser Arg Thr	
145 150 155 160	
ctg caa atg ccg ccg tac gag aaa ggc acg acg aaa cgc gtt acc ggg	528
Leu Gln Met Pro Pro Tyr Glu Lys Gly Thr Thr Lys Arg Val Thr Gly	
165 170 175	
ttt acc ctg acc ctt gaa gag gcc gta cca ttt gac atg gta gct tat	576
Phe Thr Leu Thr Leu Glu Glu Ala Val Pro Phe Asp Met Val Ala Tyr	
180 185 190	
ggt cga aac ctg atg ctg aag gct tcg gca ggt tcc ttt cca aca att	624
Gly Arg Asn Leu Met Leu Lys Ala Ser Ala Gly Ser Phe Pro Thr Ile	
195 200 205	
gac ttg ctc tat gac tac aga tcg ttt ttt gac caa tgt tcc gat att	672
Asp Leu Leu Tyr Asp Tyr Arg Ser Phe Phe Asp Gln Cys Ser Asp Ile	
210 215 220	
gga cgg atc ggc ttc ttt ccg gaa gat gtt cct aag ccg aaa gtg gcg	720
Gly Arg Ile Gly Phe Phe Pro Glu Asp Val Pro Lys Pro Lys Val Ala	
225 230 235 240	

sequence listing

atc att ggc gct ggc att tcc gga ctc gtg gta gca agc gaa ctg ctt	768
Ile Ile Gly Ala Gly Ile Ser Gly Leu Val Val Ala Ser Glu Leu Leu	
	245 250 255
cat gct ggt gta gac gat gtt aca ata tat gaa gca agt gat cgg gtt	816
His Ala Gly Val Asp Asp Val Thr Ile Tyr Glu Ala Ser Asp Arg Val	
	260 265 270
gga ggc aag ctt tgg tca cat gct ttc aag gat gct ccc agc gtg gtg	864
Gly Gly Lys Leu Trp Ser His Ala Phe Lys Asp Ala Pro Ser Val Val	
	275 280 285
gcc gaa atg ggg gcg atg cga ttt cct cct gct gca tcg tgc ttg ttt	912
Ala Glu Met Gly Ala Met Arg Phe Pro Pro Ala Ala Ser Cys Leu Phe	
	290 295 300
ttc ttc ctc gag cgg tac ggc ctg tct tcg atg agg ccg ttc cca aat	960
Phe Phe Leu Glu Arg Tyr Gly Leu Ser Ser Met Arg Pro Phe Pro Asn	
	305 310 315 320
ccc ggc aca gtc gac act aac ttg gtc tac caa ggc ctc cga tac gtg	1008
Pro Gly Thr Val Asp Thr Asn Leu Val Tyr Gln Gly Leu Arg Tyr Val	
	325 330 335
tgg aaa gcc ggg cag cag cca ccg aag ctg ttc cat cgc gtt tac agc	1056
Trp Lys Ala Gly Gln Gln Pro Pro Lys Leu Phe His Arg Val Tyr Ser	
	340 345 350
ggt tgg cgt gcg ttc ttg agg gac ggt ttc cat gag gga gat att gtg	1104
Gly Trp Arg Ala Phe Leu Arg Asp Gly Phe His Glu Gly Asp Ile Val	
	355 360 365
ttg gct tcg cct gtt gtt att act caa gcc ttg aaa tca gga gac att	1152
Leu Ala Ser Pro Val Val Ile Thr Gln Ala Leu Lys Ser Gly Asp Ile	
	370 375 380
agg cgg gct cat gac tcc tgg caa act tgg ctg aac cgt ttc ggg agg	1200
Arg Arg Ala His Asp Ser Trp Gln Thr Trp Leu Asn Arg Phe Gly Arg	
	385 390 395 400
gag tcc ttc tct tca gcg ata gag agg atc ttt ctg ggc acg cat cct	1248
Glu Ser Phe Ser Ser Ala Ile Glu Arg Ile Phe Leu Gly Thr His Pro	
	405 410 415
cct ggt ggt gaa aca tgg agt ttc cct cat gat tgg gac cta ttc aag	1296
Pro Gly Gly Glu Thr Trp Ser Phe Pro His Asp Trp Asp Leu Phe Lys	
	420 425 430
cta atg gga ata gga tct ggc ggg ttt ggt cca gtt ttt gaa agc ggg	1344
Leu Met Gly Ile Gly Ser Gly Gly Phe Gly Pro Val Phe Glu Ser Gly	
	435 440 445
ttt att gag atc ctt cgc ttg gtc ata aac gga tat gaa gaa aat cag	1392
Phe Ile Glu Ile Leu Arg Leu Val Ile Asn Gly Tyr Glu Glu Asn Gln	
	450 455 460
cgg atg tgc tct gaa gga atc tca gaa ctt cca cgt cga ata gcc tct	1440
Arg Met Cys Ser Glu Gly Ile Ser Glu Leu Pro Arg Arg Ile Ala Ser	
	465 470 475 480
caa gtg gtt aac ggt gtg tct gta agc cag cgt ata cgc cat gtt caa	1488
Gln Val Val Asn Gly Val Ser Val Ser Gln Arg Ile Arg His Val Gln	

sequence listing																	
485					490					495							
gtc	agg	gcg	att	gag	aag	gaa	aag	aca	aaa	ata	aag	ata	agg	ctt	aag		1536
Val	Arg	Ala	Ile	Glu	Lys	Glu	Lys	Thr	Lys	Ile	Lys	Ile	Arg	Leu	Lys		
			500					505					510				
agc	ggg	ata	tct	gaa	ctt	tat	gat	aag	gtg	gtg	gtt	aca	tct	gga	ctc		1584
Ser	Gly	Ile	Ser	Glu	Leu	Tyr	Asp	Lys	Val	Val	Val	Thr	Ser	Gly	Leu		
		515					520					525					
gca	aat	atc	caa	ctc	agg	cat	tgt	ctg	aca	tgc	gat	acc	acc	att	ttt		1632
Ala	Asn	Ile	Gln	Leu	Arg	His	Cys	Leu	Thr	Cys	Asp	Thr	Thr	Ile	Phe		
	530					535					540						
cgt	gca	cca	gtg	aac	caa	gcg	gtt	gat	aac	agc	cat	atg	aca	ggc	tcg		1680
Arg	Ala	Pro	Val	Asn	Gln	Ala	Val	Asp	Asn	Ser	His	Met	Thr	Gly	Ser		
545					550					555					560		
tca	aaa	ctc	ttt	ctg	ctg	act	gaa	cga	aaa	ttt	tgg	tta	gac	cat	atc		1728
Ser	Lys	Leu	Phe	Leu	Leu	Thr	Glu	Arg	Lys	Phe	Trp	Leu	Asp	His	Ile		
				565					570					575			
ctc	ccg	tcc	tgt	gtc	ctc	atg	gac	ggg	atc	gca	aaa	gca	gtg	tac	tgc		1776
Leu	Pro	Ser	Cys	Val	Leu	Met	Asp	Gly	Ile	Ala	Lys	Ala	Val	Tyr	Cys		
			580					585					590				
ttg	gac	tat	gag	ccg	cag	gat	ccg	aat	ggt	aaa	ggt	ctg	gtg	ccc	ccc		1824
Leu	Asp	Tyr	Glu	Pro	Gln	Asp	Pro	Asn	Gly	Lys	Gly	Leu	Val	Pro	Pro		
		595					600					605					
act	tat	aca	tgg	gag	gac	gac	tcc	cac	aag	ctg	ttg	gcg	gtt	ccc	gac		1872
Thr	Tyr	Thr	Trp	Glu	Asp	Asp	Ser	His	Lys	Leu	Leu	Ala	Val	Pro	Asp		
	610				615					620							
aaa	aaa	gag	cga	ttc	tgt	ctg	ctg	cgg	gac	gca	att	tcg	aga	tct	ttc		1920
Lys	Lys	Glu	Arg	Phe	Cys	Leu	Leu	Arg	Asp	Ala	Ile	Ser	Arg	Ser	Phe		
625					630					635					640		
ccg	gcg	ttt	gcc	cag	cat	cta	gtt	cct	gcc	tgc	gct	gat	tac	gac	caa		1968
Pro	Ala	Phe	Ala	Gln	His	Leu	Val	Pro	Ala	Cys	Ala	Asp	Tyr	Asp	Gln		
				645					650					655			
aat	gtt	gtt	caa	cat	gat	tgg	ctt	aca	gac	gag	aat	gcc	ggg	gga	gct		2016
Asn	Val	Val	Gln	His	Asp	Trp	Leu	Thr	Asp	Glu	Asn	Ala	Gly	Gly	Ala		
			660					665					670				
ttc	aaa	ctc	aac	cgg	cgt	ggc	gag	gat	ttt	tat	tct	gaa	gaa	ctt	ttc		2064
Phe	Lys	Leu	Asn	Arg	Arg	Gly	Glu	Asp	Phe	Tyr	Ser	Glu	Glu	Leu	Phe		
		675					680					685					
ttt	caa	gcg	ctg	gac	atg	cct	aat	gat	acc	gga	gtt	tac	ttg	gcg	ggt		2112
Phe	Gln	Ala	Leu	Asp	Met	Pro	Asn	Asp	Thr	Gly	Val	Tyr	Leu	Ala	Gly		
	690					695					700						
tgc	agt	tgt	tcc	ttc	acc	ggt	gga	tgg	gtg	gag	ggc	gct	att	cag	acc		2160
Cys	Ser	Cys	Ser	Phe	Thr	Gly	Gly	Trp	Val	Glu	Gly	Ala	Ile	Gln	Thr		
705					710					715					720		
gcg	tgt	aac	gcc	gtc	tgt	gca	att	atc	cac	aat	tgt	gga	ggt	att	ttg		2208
Ala	Cys	Asn	Ala	Val	Cys	Ala	Ile	Ile	His	Asn	Cys	Gly	Gly	Ile	Leu		
				725					730					735			
gca	aag	gac	aat	cct	ctc	gaa	cac	tct	tgg	aag	aga	tat	aac	tac	cgc		2256
Ala	Lys	Asp	Asn	Pro	Leu	Glu	His	Ser	Trp	Lys	Arg	Tyr	Asn	Tyr	Arg		

740

2268

<400> 32

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sequence listing

Gly Gly Lys Leu Trp Ser His Ala Phe Lys Asp Ala Pro Ser Val Val
275 280 285

Ala Glu Met Gly Ala Met Arg Phe Pro Pro Ala Ala Ser Cys Leu Phe
290 295 300

Phe Phe Leu Glu Arg Tyr Gly Leu Ser Ser Met Arg Pro Phe Pro Asn
305 310 315 320

Pro Gly Thr Val Asp Thr Asn Leu Val Tyr Gln Gly Leu Arg Tyr Val
325 330 335

Trp Lys Ala Gly Gln Gln Pro Pro Lys Leu Phe His Arg Val Tyr Ser
340 345 350

Gly Trp Arg Ala Phe Leu Arg Asp Gly Phe His Glu Gly Asp Ile Val
355 360 365

Leu Ala Ser Pro Val Val Ile Thr Gln Ala Leu Lys Ser Gly Asp Ile
370 375 380

Arg Arg Ala His Asp Ser Trp Gln Thr Trp Leu Asn Arg Phe Gly Arg
385 390 395 400

Glu Ser Phe Ser Ser Ala Ile Glu Arg Ile Phe Leu Gly Thr His Pro
405 410 415

Pro Gly Gly Glu Thr Trp Ser Phe Pro His Asp Trp Asp Leu Phe Lys
420 425 430

Leu Met Gly Ile Gly Ser Gly Gly Phe Gly Pro Val Phe Glu Ser Gly
435 440 445

Phe Ile Glu Ile Leu Arg Leu Val Ile Asn Gly Tyr Glu Glu Asn Gln
450 455 460

Arg Met Cys Ser Glu Gly Ile Ser Glu Leu Pro Arg Arg Ile Ala Ser
465 470 475 480

Gln Val Val Asn Gly Val Ser Val Ser Gln Arg Ile Arg His Val Gln
485 490 495

Val Arg Ala Ile Glu Lys Glu Lys Thr Lys Ile Lys Ile Arg Leu Lys
500 505 510

Ser Gly Ile Ser Glu Leu Tyr Asp Lys Val Val Val Thr Ser Gly Leu
515 520 525

Ala Asn Ile Gln Leu Arg His Cys Leu Thr Cys Asp Thr Thr Ile Phe
530 535 540

Arg Ala Pro Val Asn Gln Ala Val Asp Asn Ser His Met Thr Gly Ser
545 550 555 560

Ser Lys Leu Phe Leu Leu Thr Glu Arg Lys Phe Trp Leu Asp His Ile
565 570 575

Leu Pro Ser Cys Val Leu Met Asp Gly Ile Ala Lys Ala Val Tyr Cys
580 585 590

Leu Asp Tyr Glu Pro Gln Asp Pro Asn Gly Lys Gly Leu Val Pro Pro
595 600 605

sequence listing

Thr Tyr Thr Trp Glu Asp Asp Ser His Lys Leu Leu Ala Val Pro Asp
610 615 620
Lys Lys Glu Arg Phe Cys Leu Leu Arg Asp Ala Ile Ser Arg Ser Phe
625 630 635 640
Pro Ala Phe Ala Gln His Leu Val Pro Ala Cys Ala Asp Tyr Asp Gln
645 650 655
Asn Val Val Gln His Asp Trp Leu Thr Asp Glu Asn Ala Gly Gly Ala
660 665 670
Phe Lys Leu Asn Arg Arg Gly Glu Asp Phe Tyr Ser Glu Glu Leu Phe
675 680 685
Phe Gln Ala Leu Asp Met Pro Asn Asp Thr Gly Val Tyr Leu Ala Gly
690 695 700
Cys Ser Cys Ser Phe Thr Gly Gly Trp Val Glu Gly Ala Ile Gln Thr
705 710 715 720
Ala Cys Asn Ala Val Cys Ala Ile Ile His Asn Cys Gly Gly Ile Leu
725 730 735
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740 745 750
Asn Arg Asn
755

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<223> coding for indoleacetamide hydrolase

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aaa gac tac tcc tgc tta gaa cta gta gaa act ctg ata gcg cgt tgc 96
Lys Asp Tyr Ser Cys Leu Glu Leu Val Glu Thr Leu Ile Ala Arg Cys
20 25 30
caa gct gca aaa cca tta aat gcc ctt ctg gct aca gac tgg gat ggc 144
Gln Ala Ala Lys Pro Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Gly
35 40 45
ttg cgg cga agc gcc aaa aaa aat gat cgt cat gga aac gcc gga tta 192
Leu Arg Arg Ser Ala Lys Lys Asn Asp Arg His Gly Asn Ala Gly Leu
50 55 60
ggg ctt tgc ggc att cca ctc tgt ttt aag gcg aac atc gcg acc ggc 240
Gly Leu Cys Gly Ile Pro Leu Cys Phe Lys Ala Asn Ile Ala Thr Gly
65 70 75 80
gta ttt cct aca agc gct gct act ccg gcg ctg ata aac cac ttg cca 288
Val Phe Pro Thr Ser Ala Ala Thr Pro Ala Leu Ile Asn His Leu Pro
85 90 95

sequence listing

aag Lys	ata Ile	cca Pro	tcc Ser 100	cgc Arg	gtc Val	gca Ala	gaa Glu	aga Arg 105	ctt Leu	ttt Phe	tca Ser	gct Ala 110	gga Gly	gca Ala	ctg Leu	336
ccg Pro	ggt Gly	gcc Ala 115	tcg Ser	gga Gly	aac Asn	atg Met	cat His 120	gag Glu	tta Leu	tcg Ser	ttt Phe	gga Gly 125	att Ile	acg Thr	agc Ser	384
aac Asn 130	aac Asn	tat Tyr	gcc Ala	acc Thr	ggt Gly	gcg Ala 135	gtg Val	cgg Arg	aac Asn	ccg Pro	tgg Trp 140	aat Asn	cca Pro	agt Ser	ctg Leu	432
ata Ile 145	cca Pro	ggg Gly	ggt Gly	tca Ser	agc Ser 150	ggt Gly	ggt Gly	gtg Val	gct Ala	gct Ala 155	gcg Ala	gtg Val	gca Ala	agc Ser	cga Arg 160	480
ttg Leu	atg Met	tta Leu	ggc Gly	ggc Gly 165	ata Ile	ggc Gly	acg Thr	gat Asp	acc Thr 170	ggt Gly	gca Ala	tct Ser	gtt Val	cgc Arg 175	cta Leu	528
ccg Pro	gca Ala	gcc Ala	ctg Leu 180	tgt Cys	ggc Gly	gta Val	gta Val	gga Gly 185	ttt Phe	cga Arg	ccg Pro	acg Thr	ctt Leu 190	ggt Gly	cga Arg	576
tat Tyr	cca Pro	aga Arg 195	gat Asp	cgg Arg	ata Ile	ata Ile	ccg Pro 200	ttc Phe	agc Ser	ccc Pro	acc Thr	cgg Arg 205	gac Asp	acc Thr	gcc Ala	624
gga Gly 210	atc Ile	ata Ile	gcg Ala	cag Gln	tgc Cys	gta Val 215	gcc Ala	gat Asp	gtt Val	ata Ile	atc Ile 220	ctc Leu	gac Asp	cag Gln	gtg Val	672
att Ile 225	tcc Ser	gga Gly	cgg Arg	tcg Ser	gcg Ala 230	aaa Lys	att Ile	tca Ser	ccc Pro	atg Met 235	ccg Pro	ctg Leu	aag Lys	ggg Gly	ctt Leu 240	720
cgg Arg	atc Ile	ggc Gly	ctc Leu	ccc Pro 245	act Thr	acc Thr	tac Tyr	ttt Phe	tac Tyr 250	gat Asp	gac Asp	ctt Leu	gat Asp	gct Ala 255	gat Asp	768
gtg Val	gcc Ala	ttc Phe	gca Ala 260	gct Ala	gaa Glu	acg Thr	acg Thr	att Ile 265	cgc Arg	ttg Leu	cta Leu	gcc Ala	aac Asn 270	aga Arg	ggc Gly	816
gta Val	acc Thr	ttt Phe 275	gtt Val	gaa Glu	gcc Ala	gac Asp	atc Ile 280	ccc Pro	cac His	cta Leu	gag Glu	gaa Glu 285	ttg Leu	aac Asn	agt Ser	864
ggg Gly 290	gca Ala	agt Ser	ttg Leu	cca Pro	att Ile	gcg Ala 295	ctt Leu	tac Tyr	gaa Glu	ttt Phe	cca Pro 300	cac His	gct Ala	cta Leu	aaa Lys	912
aag Lys 305	tat Tyr	ctc Leu	gac Asp	gat Asp	ttt Phe 310	gtg Val	gga Gly	aca Thr	gtt Val	tct Ser 315	ttt Phe	tct Ser	gac Asp	gtt Val	atc Ile 320	960
aaa Lys	gga Gly	att Ile	cgt Arg	agc Ser 325	ccc Pro	gat Asp	gta Val	gcg Ala	aac Asn 330	att Ile	gtc Val	agt Ser	gcg Ala	caa Gln 335	att Ile	1008
gat Asp	ggg Gly	cat His	caa Gln	att Ile	tcc Ser	aac Asn	gat Asp	gaa Glu	tat Tyr	gaa Glu	ctg Leu	gcg Ala	cgt Arg	caa Gln	tcc Ser	1056

sequence listing

340 345 350

ttc agg cca agg ctc cag gcc act tat cgg aat tac ttc aga ctc tat	1104
Phe Arg Pro Arg Leu Gln Ala Thr Tyr Arg Asn Tyr Phe Arg Leu Tyr	
355 360 365	
cag tta gat gca atc ctt ttc cca act gca ccc tta gcg gcc aaa gcc	1152
Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Ala Ala Lys Ala	
370 375 380	
ata ggt cag gag tcg tca gtc atc cac aat ggc tca atg atg aac act	1200
Ile Gly Gln Glu Ser Ser Val Ile His Asn Gly Ser Met Met Asn Thr	
385 390 395 400	
ttc aag atc tac gtg cga aat gtg gac cca agc agc aac gca ggc cta	1248
Phe Lys Ile Tyr Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu	
405 410 415	
cct ggg ttg agc ctt cct gcc tgc ctt aca cct gat cgc ttg cct gtt	1296
Pro Gly Leu Ser Leu Pro Ala Cys Leu Thr Pro Asp Arg Leu Pro Val	
420 425 430	
gga atg gaa att gat gga tta gcg ggg tca gac cac cgt ctg tta gca	1344
Gly Met Glu Ile Asp Gly Leu Ala Gly Ser Asp His Arg Leu Leu Ala	
435 440 445	
atc ggg gca gca tta gaa aaa gct ata aat ttt tct tcc ttt ccc gat	1392
Ile Gly Ala Ala Leu Glu Lys Ala Ile Asn Phe Ser Ser Phe Pro Asp	
450 455 460	
gct ttt aat tag	1404
Ala Phe Asn	
465	

<210> 34
 <211> 467
 <212> PRT
 <213> Agrobacterium tumefaciens

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 1 5 10 15
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 20 25 30
 Gln Ala Ala Lys Pro Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Gly
 35 40 45
 Leu Arg Arg Ser Ala Lys Lys Asn Asp Arg His Gly Asn Ala Gly Leu
 50 55 60
 Gly Leu Cys Gly Ile Pro Leu Cys Phe Lys Ala Asn Ile Ala Thr Gly
 65 70 75 80
 Val Phe Pro Thr Ser Ala Ala Thr Pro Ala Leu Ile Asn His Leu Pro
 85 90 95
 Lys Ile Pro Ser Arg Val Ala Glu Arg Leu Phe Ser Ala Gly Ala Leu
 100 105 110
 Pro Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser

sequence listing

115	120	125
Asn Asn Tyr Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu	130	140
Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Ala Val Ala Ser Arg	145	155
Leu Met Leu Gly Gly Ile Gly Thr Asp Thr Gly Ala Ser Val Arg Leu	165	170
Pro Ala Ala Leu Cys Gly Val Val Gly Phe Arg Pro Thr Leu Gly Arg	180	190
Tyr Pro Arg Asp Arg Ile Ile Pro Phe Ser Pro Thr Arg Asp Thr Ala	195	205
Gly Ile Ile Ala Gln Cys Val Ala Asp Val Ile Ile Leu Asp Gln Val	210	220
Ile Ser Gly Arg Ser Ala Lys Ile Ser Pro Met Pro Leu Lys Gly Leu	225	235
Arg Ile Gly Leu Pro Thr Thr Tyr Phe Tyr Asp Asp Leu Asp Ala Asp	245	255
Val Ala Phe Ala Ala Glu Thr Thr Ile Arg Leu Leu Ala Asn Arg Gly	260	270
Val Thr Phe Val Glu Ala Asp Ile Pro His Leu Glu Glu Leu Asn Ser	275	285
Gly Ala Ser Leu Pro Ile Ala Leu Tyr Glu Phe Pro His Ala Leu Lys	290	300
Lys Tyr Leu Asp Asp Phe Val Gly Thr Val Ser Phe Ser Asp Val Ile	305	315
Lys Gly Ile Arg Ser Pro Asp Val Ala Asn Ile Val Ser Ala Gln Ile	325	330
Asp Gly His Gln Ile Ser Asn Asp Glu Tyr Glu Leu Ala Arg Gln Ser	340	345
Phe Arg Pro Arg Leu Gln Ala Thr Tyr Arg Asn Tyr Phe Arg Leu Tyr	355	360
Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Ala Ala Lys Ala	370	375
Ile Gly Gln Glu Ser Ser Val Ile His Asn Gly Ser Met Met Asn Thr	385	390
Phe Lys Ile Tyr Val Arg Asn Val Asp Pro Ser Ser Asn Ala Gly Leu	405	410
Pro Gly Leu Ser Leu Pro Ala Cys Leu Thr Pro Asp Arg Leu Pro Val	420	425
Gly Met Glu Ile Asp Gly Leu Ala Gly Ser Asp His Arg Leu Leu Ala	435	440
Ile Gly Ala Ala Leu Glu Lys Ala Ile Asn Phe Ser Phe Pro Asp		

sequence listing
460

450

455

Ala Phe Asn
465

<210> 35
<211> 1419
<212> DNA
<213> Agrobacterium vitis
<220>
<221> CDS
<222> (1)..(1416)
<223> coding for indoleacetamide hydrolase

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  1                    5              10              15

aaa aaa tac tcc tgt tcc gaa ctg gct gaa acc ata ata gcc cgt tgc 96
Lys Lys Tyr Ser Cys Ser Glu Leu Ala Glu Thr Ile Ile Ala Arg Cys
                    20              25              30

gaa gcc gcg aaa tct ctc aat gct ctt ctg gcg act gac tgg gat tac 144
Glu Ala Ala Lys Ser Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Tyr
                    35              40              45

ctg cgg cgt aat gcc aag aaa gta gat gaa gat gga agc gcc ggc gag 192
Leu Arg Arg Asn Ala Lys Lys Val Asp Glu Asp Gly Ser Ala Gly Glu
                    50              55              60

ggt ctt gcc ggc atc ccg ctg tgt tct aaa gcg aac att gca aca ggc 240
Gly Leu Ala Gly Ile Pro Leu Cys Ser Lys Ala Asn Ile Ala Thr Gly
  65              70              75              80

ata ttc cca gca agc gcg gcc acg ccg gcg ctt gat gaa cat tta cct 288
Ile Phe Pro Ala Ser Ala Ala Thr Pro Ala Leu Asp Glu His Leu Pro
                    85              90              95

aca aca cca gcc ggc gtc cgt aaa ccg ctt cta gac gct ggg gca ctg 336
Thr Thr Pro Ala Gly Val Arg Lys Pro Leu Leu Asp Ala Gly Ala Leu
                    100              105              110

ata ggc gct tcg gga aac atg cat gag tta tcg ttt ggc att acc agt 384
Ile Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser
                    115              120              125

aac aac cac gcc act ggt gcg gtg aga aac ccc tgg aat ccc agc tta 432
Asn Asn His Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu
                    130              135              140

ata cca gga ggc tcg agc ggc ggc gtg gct gct gct gta gca tca cgg 480
Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Val Ala Ser Arg
  145              150              155              160

tta atg ctc ggc gga att ggc acc gac acg ggg gct tcg gtc cgc cta 528
Leu Met Leu Gly Gly Ile Gly Thr Asp Thr Gly Ala Ser Val Arg Leu
                    165              170              175

cct gca tcc cta tgt ggc gta gtg gga ttc cgc ccg acg atc ggc aga 576
Pro Ala Ser Leu Cys Gly Val Val Gly Phe Arg Pro Thr Ile Gly Arg
                    180              185              190

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sequence listing

tat cct gga gac cga att gtg ccg gtt agc ccc acc cgc gat aca gcc	624
Tyr Pro Gly Asp Arg Ile Val Pro Val Ser Pro Thr Arg Asp Thr Ala	
195 200 205	
gga att atc gca cag agc gtt cct gat gtg ata ctc ctt gac caa atc	672
Gly Ile Ile Ala Gln Ser Val Pro Asp Val Ile Leu Leu Asp Gln Ile	
210 215 220	
att tgc ggg aag ctc acg acc cac caa cct gta ccc ctg gag gga tta	720
Ile Cys Gly Lys Leu Thr Thr His Gln Pro Val Pro Leu Glu Gly Leu	
225 230 235	
cgt atc ggc ttg cca acc act tac ttt tac gat gac ctt gat gct gat	768
Arg Ile Gly Leu Pro Thr Thr Tyr Phe Tyr Asp Asp Leu Asp Ala Asp	
245 250 255	
gtg gcc ttc gca gct gaa aac ctt atc acg ctg ctg gcc agc aag ggt	816
Val Ala Phe Ala Ala Glu Asn Leu Ile Thr Leu Leu Ala Ser Lys Gly	
260 265 270	
gta acc ttt gtt aag gcc gag att cca gat ctg cag cgt ctg aac atc	864
Val Thr Phe Val Lys Ala Glu Ile Pro Asp Leu Gln Arg Leu Asn Ile	
275 280 285	
ggg gtt agc ttt cct att gcc ctg tac gag ttt ccg ttc gcc cta caa	912
Gly Val Ser Phe Pro Ile Ala Leu Tyr Glu Phe Pro Phe Ala Leu Gln	
290 295 300	
aag tat atc gat gac ttt gtg aag gat gtg tct ttt tct gac gtc atc	960
Lys Tyr Ile Asp Asp Phe Val Lys Asp Val Ser Phe Ser Asp Val Ile	
305 310 315 320	
aaa gga att cgt agc cct gat gta gcc aac att gcc aat gct caa att	1008
Lys Gly Ile Arg Ser Pro Asp Val Ala Asn Ile Ala Asn Ala Gln Ile	
325 330 335	
gat gga cat caa att tcc aaa gct tca tat gaa ctg gcg cga caa tct	1056
Asp Gly His Gln Ile Ser Lys Ala Ser Tyr Glu Leu Ala Arg Gln Ser	
340 345 350	
ttc aga cca aag ctg caa gcc gcc tac cat gat tac ttc aag ctg cac	1104
Phe Arg Pro Lys Leu Gln Ala Ala Tyr His Asp Tyr Phe Lys Leu His	
355 360 365	
cag cta gac gcg atc ctt ttc ccg aca gct ccc ctg aca gcc aaa ccg	1152
Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Thr Ala Lys Pro	
370 375 380	
atc ggc caa gat tta tcg gtg atg cac aat ggc gta atg gcc gac acg	1200
Ile Gly Gln Asp Leu Ser Val Met His Asn Gly Val Met Ala Asp Thr	
385 390 395 400	
ttt aaa atc ttc gtg cga aat gtg gat ccg ggg agc aac gca ggc ctg	1248
Phe Lys Ile Phe Val Arg Asn Val Asp Pro Gly Ser Asn Ala Gly Leu	
405 410 415	
cca gga tta agc ctt ccc gtt tct ctt act tca aag ggt ttg cct att	1296
Pro Gly Leu Ser Leu Pro Val Ser Leu Thr Ser Lys Gly Leu Pro Ile	
420 425 430	
gga atg gaa atc gat gga tta gcg ggc atg gac gac cgt ttg cta gca	1344
Gly Met Glu Ile Asp Gly Leu Ala Gly Met Asp Asp Arg Leu Leu Ala	

sequence listing

435	440	445	
atc gga gcg gca cta gag gaa gcg ata gct ttt cat aat tta cct gac			1392
Ile Gly Ala Ala Leu Glu Glu Ala Ile Ala Phe His Asn Leu Pro Asp			
450	455	460	
ttc ccg aaa gtc gag aca aac tac tga			1419
Phe Pro Lys Val Glu Thr Asn Tyr			
465	470		

<210> 36
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 <212> PRT
 <213> Agrobacterium vitis

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 Lys Lys Tyr Ser Cys Ser Glu Leu Ala Glu Thr Ile Ile Ala Arg Cys
 20 25 30
 Glu Ala Ala Lys Ser Leu Asn Ala Leu Leu Ala Thr Asp Trp Asp Tyr
 35 40 45
 Leu Arg Arg Asn Ala Lys Lys Val Asp Glu Asp Gly Ser Ala Gly Glu
 50 55 60
 Gly Leu Ala Gly Ile Pro Leu Cys Ser Lys Ala Asn Ile Ala Thr Gly
 65 70 75 80
 Ile Phe Pro Ala Ser Ala Ala Thr Pro Ala Leu Asp Glu His Leu Pro
 85 90 95
 Thr Thr Pro Ala Gly Val Arg Lys Pro Leu Leu Asp Ala Gly Ala Leu
 100 105 110
 Ile Gly Ala Ser Gly Asn Met His Glu Leu Ser Phe Gly Ile Thr Ser
 115 120 125
 Asn Asn His Ala Thr Gly Ala Val Arg Asn Pro Trp Asn Pro Ser Leu
 130 135 140
 Ile Pro Gly Gly Ser Ser Gly Gly Val Ala Ala Ala Val Ala Ser Arg
 145 150 155 160
 Leu Met Leu Gly Gly Ile Gly Thr Asp Thr Gly Ala Ser Val Arg Leu
 165 170 175
 Pro Ala Ser Leu Cys Gly Val Val Gly Phe Arg Pro Thr Ile Gly Arg
 180 185 190
 Tyr Pro Gly Asp Arg Ile Val Pro Val Ser Pro Thr Arg Asp Thr Ala
 195 200 205
 Gly Ile Ile Ala Gln Ser Val Pro Asp Val Ile Leu Leu Asp Gln Ile
 210 215 220
 Ile Cys Gly Lys Leu Thr Thr His Gln Pro Val Pro Leu Glu Gly Leu
 225 230 235 240
 Arg Ile Gly Leu Pro Thr Thr Tyr Phe Tyr Asp Asp Leu Asp Ala Asp

sequence listing

245	250	255
Val Ala Phe Ala Ala Glu Asn Leu Ile Thr Leu Leu Ala Ser Lys Gly		
260	265	270
Val Thr Phe Val Lys Ala Glu Ile Pro Asp Leu Gln Arg Leu Asn Ile		
275	280	285
Gly Val Ser Phe Pro Ile Ala Leu Tyr Glu Phe Pro Phe Ala Leu Gln		
290	295	300
Lys Tyr Ile Asp Asp Phe Val Lys Asp Val Ser Phe Ser Asp Val Ile		
305	310	315
Lys Gly Ile Arg Ser Pro Asp Val Ala Asn Ile Ala Asn Ala Gln Ile		
325	330	335
Asp Gly His Gln Ile Ser Lys Ala Ser Tyr Glu Leu Ala Arg Gln Ser		
340	345	350
Phe Arg Pro Lys Leu Gln Ala Ala Tyr His Asp Tyr Phe Lys Leu His		
355	360	365
Gln Leu Asp Ala Ile Leu Phe Pro Thr Ala Pro Leu Thr Ala Lys Pro		
370	375	380
Ile Gly Gln Asp Leu Ser Val Met His Asn Gly Val Met Ala Asp Thr		
385	390	395
Phe Lys Ile Phe Val Arg Asn Val Asp Pro Gly Ser Asn Ala Gly Leu		
405	410	415
Pro Gly Leu Ser Leu Pro Val Ser Leu Thr Ser Lys Gly Leu Pro Ile		
420	425	430
Gly Met Glu Ile Asp Gly Leu Ala Gly Met Asp Asp Arg Leu Leu Ala		
435	440	445
Ile Gly Ala Ala Leu Glu Glu Ala Ile Ala Phe His Asn Leu Pro Asp		
450	455	460
Phe Pro Lys Val Glu Thr Asn Tyr		
465	470	

<210> 37
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 <212> DNA
 <213> Arabidopsis thaliana
 <220>
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 <222> (1)..(1260)
 <223> coding for 5-methylthioribose kinase

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1	5	10
tac atc aag tca aca cct gct ctc tct tcc aag atc gga gcc gac aag		96
Tyr Ile Lys Ser Thr Pro Ala Leu Ser Ser Lys Ile Gly Ala Asp Lys		
20	25	30

sequence listing

tcc gat gat gat ttg gtt atc aaa gaa gtt gga gat ggc aat ctc aat	144
Ser Asp Asp Asp Leu Val Ile Lys Glu Val Gly Asp Gly Asn Leu Asn	
35 40 45	
ttc gtt ttc atc gtt gtt gga tcc tct ggt tct ctt gtc atc aaa cag	192
Phe Val Phe Ile Val Val Gly Ser Ser Gly Ser Leu Val Ile Lys Gln	
50 55 60	
gct ctt cca tat att cgc tgt atc ggt gaa tca tgg cca atg acg aaa	240
Ala Leu Pro Tyr Ile Arg Cys Ile Gly Glu Ser Trp Pro Met Thr Lys	
65 70 75 80	
gaa aga gct tat ttt gaa gca aca act ttg aga aag cat gga aat tta	288
Glu Arg Ala Tyr Phe Glu Ala Thr Thr Leu Arg Lys His Gly Asn Leu	
85 90 95	
tca cct gat cat gtt cct gaa gtc tac cat ttt gac aga aca atg gcg	336
Ser Pro Asp His Val Pro Glu Val Tyr His Phe Asp Arg Thr Met Ala	
100 105 110	
ttg att gga atg aga tac ctt gag cct cct cat atc att ctc cgc aaa	384
Leu Ile Gly Met Arg Tyr Leu Glu Pro Pro His Ile Ile Leu Arg Lys	
115 120 125	
gga ctc att gct ggg att gag tat cct ttc ctc gca gac cac atg tct	432
Gly Leu Ile Ala Gly Ile Glu Tyr Pro Phe Leu Ala Asp His Met Ser	
130 135 140	
gat tac atg gcg aag act ctc ttc ttc act tct ctc ctc tat cac gat	480
Asp Tyr Met Ala Lys Thr Leu Phe Phe Thr Ser Leu Leu Tyr His Asp	
145 150 155 160	
acc aca gag cac aga aga gca gta acc gaa ttt tgt ggt aat gtg gag	528
Thr Thr Glu His Arg Arg Ala Val Thr Glu Phe Cys Gly Asn Val Glu	
165 170 175	
tta tgc cga tta acg gag caa gtt gtg ttt tcg gac cca tat aga gtt	576
Leu Cys Arg Leu Thr Glu Gln Val Val Phe Ser Asp Pro Tyr Arg Val	
180 185 190	
tcc aca ttt aat cgt tgg act tca cct tat ctt gat gat gat gct aag	624
Ser Thr Phe Asn Arg Trp Thr Ser Pro Tyr Leu Asp Asp Asp Ala Lys	
195 200 205	
gct gtg cgc gaa gac agt gcc ttg aag ctc gaa atc gca gag cta aaa	672
Ala Val Arg Glu Asp Ser Ala Leu Lys Leu Glu Ile Ala Glu Leu Lys	
210 215 220	
tcg atg ttc tgt gaa aga gct caa gct tta ata cat ggt gat ctt cat	720
Ser Met Phe Cys Glu Arg Ala Gln Ala Leu Ile His Gly Asp Leu His	
225 230 235 240	
act ggt tct gtc atg gtt act caa gat tca acg caa gtt ata gat cca	768
Thr Gly Ser Val Met Val Thr Gln Asp Ser Thr Gln Val Ile Asp Pro	
245 250 255	
gag ttt tcg ttc tat gga ccg atg ggt ttc gat att ggc gct tat ctt	816
Glu Phe Ser Phe Tyr Gly Pro Met Gly Phe Asp Ile Gly Ala Tyr Leu	
260 265 270	
ggt aac ttg ata cta gct ttc ttt gca caa gat gga cac gcc act cag	864
Gly Asn Leu Ile Leu Ala Phe Phe Ala Gln Asp Gly His Ala Thr Gln	

sequence listing

275	280	285	
gaa aat gat cga aaa gaa tac aag cag tgg atc ttg aga acc att gag Glu Asn Asp Arg Lys Glu Tyr Lys Gln Trp Ile Leu Arg Thr Ile Glu 290 295 300			912
caa act tgg aat ttg ttt aac aaa agg ttc att gcg cta tgg gat caa Gln Thr Trp Asn Leu Phe Asn Lys Arg Phe Ile Ala Leu Trp Asp Gln 305 310 315 320			960
aac aaa gat gga cca ggc gaa gca tac ctt gca gat atc tat aac aat Asn Lys Asp Gly Pro Gly Glu Ala Tyr Leu Ala Asp Ile Tyr Asn Asn 325 330 335			1008
acc gag gtt ttg aag ttt gtt caa gaa aac tac atg agg aat ttg ttg Thr Glu Val Leu Lys Phe Val Gln Glu Asn Tyr Met Arg Asn Leu Leu 340 345 350			1056
cat gac tca ctc gga ttc ggc gct gca aag atg att agg aga att gtg His Asp Ser Leu Gly Phe Gly Ala Ala Lys Met Ile Arg Arg Ile Val 355 360 365			1104
gga gtg gca cat gtt gag gac ttt gaa tca atc gaa gaa gat aag cga Gly Val Ala His Val Glu Asp Phe Glu Ser Ile Glu Glu Asp Lys Arg 370 375 380			1152
aga gct att tgc gag aga agt gca ctc gag ttt gcg aag atg ctt ctc Arg Ala Ile Cys Glu Arg Ser Ala Leu Glu Phe Ala Lys Met Leu Leu 385 390 395 400			1200
aag gaa agg aga aag ttt aag agt atc ggt gaa gtt gtt tca gca att Lys Glu Arg Arg Lys Phe Lys Ser Ile Gly Glu Val Val Ser Ala Ile 405 410 415			1248
caa caa caa agc taa Gln Gln Gln Ser 420			1263

<210> 38

<211> 420

<212> PRT

<213> Arabidopsis thaliana

<400> 38

Met Ser Phe Glu Glu Phe Thr Pro Leu Asn Glu Lys Ser Leu Val Asp
1 5 10 15

Tyr Ile Lys Ser Thr Pro Ala Leu Ser Ser Lys Ile Gly Ala Asp Lys
20 25 30

Ser Asp Asp Asp Leu Val Ile Lys Glu Val Gly Asp Gly Asn Leu Asn
35 40 45

Phe Val Phe Ile Val Val Gly Ser Ser Gly Ser Leu Val Ile Lys Gln
50 55 60

Ala Leu Pro Tyr Ile Arg Cys Ile Gly Glu Ser Trp Pro Met Thr Lys
65 70 75 80

Glu Arg Ala Tyr Phe Glu Ala Thr Thr Leu Arg Lys His Gly Asn Leu
85 90 95

Ser Pro Asp His Val Pro Glu Val Tyr His Phe Asp Arg Thr Met Ala

sequence listing

100	105	110
Leu Ile Gly Met Arg Tyr Leu Glu	Pro Pro His Ile Ile	Leu Arg Lys
115	120	125
Gly Leu Ile Ala Gly Ile Glu Tyr Pro Phe Leu Ala Asp His Met Ser		
130	135	140
Asp Tyr Met Ala Lys Thr Leu Phe Phe Thr Ser Leu Leu Tyr His Asp		
145	150	155
Thr Thr Glu His Arg Arg Ala Val Thr Glu Phe Cys Gly Asn Val Glu		
165	170	175
Leu Cys Arg Leu Thr Glu Gln Val Val Phe Ser Asp Pro Tyr Arg Val		
180	185	190
Ser Thr Phe Asn Arg Trp Thr Ser Pro Tyr Leu Asp Asp Asp Ala Lys		
195	200	205
Ala Val Arg Glu Asp Ser Ala Leu Lys Leu Glu Ile Ala Glu Leu Lys		
210	215	220
Ser Met Phe Cys Glu Arg Ala Gln Ala Leu Ile His Gly Asp Leu His		
225	230	235
Thr Gly Ser Val Met Val Thr Gln Asp Ser Thr Gln Val Ile Asp Pro		
245	250	255
Glu Phe Ser Phe Tyr Gly Pro Met Gly Phe Asp Ile Gly Ala Tyr Leu		
260	265	270
Gly Asn Leu Ile Leu Ala Phe Phe Ala Gln Asp Gly His Ala Thr Gln		
275	280	285
Glu Asn Asp Arg Lys Glu Tyr Lys Gln Trp Ile Leu Arg Thr Ile Glu		
290	295	300
Gln Thr Trp Asn Leu Phe Asn Lys Arg Phe Ile Ala Leu Trp Asp Gln		
305	310	315
Asn Lys Asp Gly Pro Gly Glu Ala Tyr Leu Ala Asp Ile Tyr Asn Asn		
325	330	335
Thr Glu Val Leu Lys Phe Val Gln Glu Asn Tyr Met Arg Asn Leu Leu		
340	345	350
His Asp Ser Leu Gly Phe Gly Ala Ala Lys Met Ile Arg Arg Ile Val		
355	360	365
Gly Val Ala His Val Glu Asp Phe Glu Ser Ile Glu Glu Asp Lys Arg		
370	375	380
Arg Ala Ile Cys Glu Arg Ser Ala Leu Glu Phe Ala Lys Met Leu Leu		
385	390	395
Lys Glu Arg Arg Lys Phe Lys Ser Ile Gly Glu Val Val Ser Ala Ile		
405	410	415
Gln Gln Gln Ser		
420		

sequence listing

<211> 1200

<212> DNA

<213> *Klebsiella pneumoniae*

<220>

<221> CDS

<222> (1)..(1197)

<223> coding for 5-methylthioribose kinase

<400> 39

atg	tcg	caa	tac	cat	acc	ttc	acc	gcc	cac	gat	gcc	gtg	gct	tac	gcg	48
Met	Ser	Gln	Tyr	His	Thr	Phe	Thr	Ala	His	Asp	Ala	Val	Ala	Tyr	Ala	
1				5				10					15			

caa	cag	ttc	gcc	ggc	atc	gac	aac	cca	tct	gag	ctg	gtc	agc	gcg	cag	96
Gln	Gln	Phe	Ala	Gly	Ile	Asp	Asn	Pro	Ser	Glu	Leu	Val	Ser	Ala	Gln	
			20					25					30			

gaa	gtg	ggc	gat	ggc	aac	ctc	aat	ctg	gtg	ttt	aaa	gtg	ttc	gat	cgt	144
Glu	Val	Gly	Asp	Gly	Asn	Leu	Asn	Leu	Val	Phe	Lys	Val	Phe	Asp	Arg	
		35					40					45				

cag	ggc	gtc	agc	cgg	gcg	atc	gtc	aaa	cag	gcc	ctg	ccc	tac	gtg	cgc	192
Gln	Gly	Val	Ser	Arg	Ala	Ile	Val	Lys	Gln	Ala	Leu	Pro	Tyr	Val	Arg	
	50					55					60					

tgc	gtc	ggc	gaa	tcc	tgg	ccg	ctg	acc	ctc	gac	cgc	gcc	cgt	ctc	gaa	240
Cys	Val	Gly	Glu	Ser	Trp	Pro	Leu	Thr	Leu	Asp	Arg	Ala	Arg	Leu	Glu	
65					70					75					80	

gcg	cag	acc	ctg	gtc	gcc	cac	tat	cag	cac	agc	ccg	cag	cac	acg	gta	288
Ala	Gln	Thr	Leu	Val	Ala	His	Tyr	Gln	His	Ser	Pro	Gln	His	Thr	Val	
				85					90					95		

aaa	atc	cat	cac	ttt	gat	ccc	gag	ctg	gcg	gtg	atg	gtg	atg	gaa	gat	336
Lys	Ile	His	His	Phe	Asp	Pro	Glu	Leu	Ala	Val	Met	Val	Met	Glu	Asp	
			100					105					110			

ctt	tcc	gac	cac	cgc	atc	tgg	cgc	gga	gag	ctt	atc	gct	aac	gtc	tac	384
Leu	Ser	Asp	His	Arg	Ile	Trp	Arg	Gly	Glu	Leu	Ile	Ala	Asn	Val	Tyr	
		115					120					125				

tat	ccc	cag	gcg	gcc	cgc	cag	ctt	ggc	gac	tat	ctg	gcg	cag	gtg	ttg	432
Tyr	Pro	Gln	Ala	Ala	Arg	Gln	Leu	Gly	Asp	Tyr	Leu	Ala	Gln	Val	Leu	
	130					135					140					

ttc	cac	acc	agc	gat	ttc	tac	ctc	cat	ccc	cac	gag	aaa	aag	gcg	cag	480
Phe	His	Thr	Ser	Asp	Phe	Tyr	Leu	His	Pro	His	Glu	Lys	Lys	Ala	Gln	
145				150						155					160	

gtg	gcg	cag	ttt	att	aac	ccg	gcg	atg	tgc	gag	atc	acc	gag	gat	ctg	528
Val	Ala	Gln	Phe	Ile	Asn	Pro	Ala	Met	Cys	Glu	Ile	Thr	Glu	Asp	Leu	
			165						170					175		

ttc	ttt	aac	gac	ccg	tat	cag	atc	cac	gag	cgc	aat	aac	tac	ccg	gcg	576
Phe	Phe	Asn	Asp	Pro	Tyr	Gln	Ile	His	Glu	Arg	Asn	Asn	Tyr	Pro	Ala	
			180					185					190			

gag	ctg	gag	gcc	gat	gtc	gcc	gcc	ctg	cgc	gac	gac	gcc	cag	ctt	aag	624
Glu	Leu	Glu	Ala	Asp	Val	Ala	Ala	Leu	Arg	Asp	Asp	Ala	Gln	Leu	Lys	
		195				200						205				

ctg	gcg	gtg	gcg	gcg	ctg	aag	cac	cgt	ttc	ttt	gcc	cat	gcg	gaa	gcg	672
Leu	Ala	Val	Ala	Ala	Leu	Lys	His	Arg	Phe	Phe	Ala	His	Ala	Glu	Ala	

sequence listing
220

210	215	220		
ctg ctg cac ggc gat atc cac agc ggg tcg atc ttc gtt gcc gaa ggt Leu Leu His Gly Asp Ile His Ser Gly Ser Ile Phe Val Ala Glu Gly 225 230 235 240				720
agc ctg aag gcc atc gac gcc gag ttc ggc tac ttc ggc ccc atc ggc Ser Leu Lys Ala Ile Asp Ala Glu Phe Gly Tyr Phe Gly Pro Ile Gly 245 250 255				768
ttc gat atc ggc acc gcc atc ggc aac ctg ctg ctg aac tac tgc ggc Phe Asp Ile Gly Thr Ala Ile Gly Asn Leu Leu Leu Asn Tyr Cys Gly 260 265 270				816
ctg ccg ggc cag ctc ggc att cgc gat gcc gcc gcc gcg cgc gag cag Leu Pro Gly Gln Leu Gly Ile Arg Asp Ala Ala Ala Ala Arg Glu Gln 275 280 285				864
cgg ctg aac gac atc cac cag ctg tgg acc acc ttc gcc gag cgc ttc Arg Leu Asn Asp Ile His Gln Leu Trp Thr Thr Phe Ala Glu Arg Phe 290 295 300				912
cag gcg ctg gcg gcg gag aaa acc cgc gac gcg gcg ctg gct tac ccc Gln Ala Leu Ala Ala Glu Lys Thr Arg Asp Ala Ala Leu Ala Tyr Pro 305 310 315 320				960
ggc tac gcc tcc gcc ttt ctg aag aaa gtc tgg gcg gac gcg gtc ggc Gly Tyr Ala Ser Ala Phe Leu Lys Lys Val Trp Ala Asp Ala Val Gly 325 330 335				1008
ttc tgc ggc agc gaa ctg atc cgc cgc agc gtc gga ctg tcg cac gtc Phe Cys Gly Ser Glu Leu Ile Arg Arg Ser Val Gly Leu Ser His Val 340 345 350				1056
gcg gat atc gac act atc cag gac gac gcc atg cgt cat gag tgc ctg Ala Asp Ile Asp Thr Ile Gln Asp Asp Ala Met Arg His Glu Cys Leu 355 360 365				1104
cgc cac gcc att acc ctg ggc aga gcg ctg atc gtg ctg gcc gag cgt Arg His Ala Ile Thr Leu Gly Arg Ala Leu Ile Val Leu Ala Glu Arg 370 375 380				1152
atc gac agc gtc gac gag ctg ctg gcg cgg gta cgc cag tac agc tga Ile Asp Ser Val Asp Glu Leu Leu Ala Arg Val Arg Gln Tyr Ser 385 390 395				1200

<210> 40
 <211> 399
 <212> PRT
 <213> Klebsiella pneumoniae

<400> 40
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 Gln Gln Phe Ala Gly Ile Asp Asn Pro Ser Glu Leu Val Ser Ala Gln
 20 25 30
 Glu Val Gly Asp Gly Asn Leu Asn Leu Val Phe Lys Val Phe Asp Arg
 35 40 45
 Gln Gly Val Ser Arg Ala Ile Val Lys Gln Ala Leu Pro Tyr Val Arg
 50 55 60

sequence listing

Cys Val Gly Glu Ser Trp Pro Leu Thr Leu Asp Arg Ala Arg Leu Glu
 65 70 75 80
 Ala Gln Thr Leu Val Ala His Tyr Gln His Ser Pro Gln His Thr Val
 85 90 95
 Lys Ile His His Phe Asp Pro Glu Leu Ala Val Met Val Met Glu Asp
 100 105 110
 Leu Ser Asp His Arg Ile Trp Arg Gly Glu Leu Ile Ala Asn Val Tyr
 115 120 125
 Tyr Pro Gln Ala Ala Arg Gln Leu Gly Asp Tyr Leu Ala Gln Val Leu
 130 135 140
 Phe His Thr Ser Asp Phe Tyr Leu His Pro His Glu Lys Lys Ala Gln
 145 150 155 160
 Val Ala Gln Phe Ile Asn Pro Ala Met Cys Glu Ile Thr Glu Asp Leu
 165 170 175
 Phe Phe Asn Asp Pro Tyr Gln Ile His Glu Arg Asn Asn Tyr Pro Ala
 180 185 190
 Glu Leu Glu Ala Asp Val Ala Ala Leu Arg Asp Asp Ala Gln Leu Lys
 195 200 205
 Leu Ala Val Ala Ala Leu Lys His Arg Phe Phe Ala His Ala Glu Ala
 210 215 220
 Leu Leu His Gly Asp Ile His Ser Gly Ser Ile Phe Val Ala Glu Gly
 225 230 235 240
 Ser Leu Lys Ala Ile Asp Ala Glu Phe Gly Tyr Phe Gly Pro Ile Gly
 245 250 255
 Phe Asp Ile Gly Thr Ala Ile Gly Asn Leu Leu Leu Asn Tyr Cys Gly
 260 265 270
 Leu Pro Gly Gln Leu Gly Ile Arg Asp Ala Ala Ala Ala Arg Glu Gln
 275 280 285
 Arg Leu Asn Asp Ile His Gln Leu Trp Thr Thr Phe Ala Glu Arg Phe
 290 295 300
 Gln Ala Leu Ala Ala Glu Lys Thr Arg Asp Ala Ala Leu Ala Tyr Pro
 305 310 315 320
 Gly Tyr Ala Ser Ala Phe Leu Lys Lys Val Trp Ala Asp Ala Val Gly
 325 330 335
 Phe Cys Gly Ser Glu Leu Ile Arg Arg Ser Val Gly Leu Ser His Val
 340 345 350
 Ala Asp Ile Asp Thr Ile Gln Asp Asp Ala Met Arg His Glu Cys Leu
 355 360 365
 Arg His Ala Ile Thr Leu Gly Arg Ala Leu Ile Val Leu Ala Glu Arg
 370 375 380
 Ile Asp Ser Val Asp Glu Leu Leu Ala Arg Val Arg Gln Tyr Ser
 385 390 395

sequence listing

<210> 41
 <211> 1140
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
 <221> CDS
 <222> (1)..(1137)
 <223> coding for alcohol dehydrogenase

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gaa gcc gga aag cca ctg gtg atc gag gaa gtg gag gtt gct cca ccg 96
Glu Ala Gly Lys Pro Leu Val Ile Glu Glu Val Glu Val Ala Pro Pro
          20          25          30

cag aaa cac gaa gtt cgt atc aag att ctc ttc act tct ctc tgt cac 144
Gln Lys His Glu Val Arg Ile Lys Ile Leu Phe Thr Ser Leu Cys His
          35          40          45

acc gat gtt tac ttc tgg gaa gct aag gga caa aca ccg ttg ttt cca 192
Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Leu Phe Pro
          50          55          60

cgt atc ttc ggc cat gaa gct gga ggg att gtt gag agt gtt gga gaa 240
Arg Ile Phe Gly His Glu Ala Gly Gly Ile Val Glu Ser Val Gly Glu
  65          70          75          80

gga gtg act gat ctt cag cca gga gat cat gtg ttg ccg atc ttt acc 288
Gly Val Thr Asp Leu Gln Pro Gly Asp His Val Leu Pro Ile Phe Thr
          85          90          95

gga gaa tgt gga gat tgt cgt cat tgc cag tcg gag gaa tca aac atg 336
Gly Glu Cys Gly Asp Cys Arg His Cys Gln Ser Glu Glu Ser Asn Met
          100          105          110

tgt gat ctt ctc agg atc aac aca gag cga gga ggt atg att cac gat 384
Cys Asp Leu Leu Arg Ile Asn Thr Glu Arg Gly Gly Met Ile His Asp
          115          120          125

ggt gaa tct aga ttc tcc att aat ggc aaa cca atc tac cat ttc ctt 432
Gly Glu Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Leu
          130          135          140

ggg acg tcc acg ttc agt gag tac act gtg gtt cac tct ggt cag gtc 480
Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Val His Ser Gly Gln Val
          145          150          155          160

gct aag atc aat ccg gat gct cct ctt gac aag gtc tgt att gtc agt 528
Ala Lys Ile Asn Pro Asp Ala Pro Leu Asp Lys Val Cys Ile Val Ser
          165          170          175

tgt ggt ttg tct act ggg tta gga gca act ttg aat gtg gct aaa ccc 576
Cys Gly Leu Ser Thr Gly Leu Gly Ala Thr Leu Asn Val Ala Lys Pro
          180          185          190

aag aaa ggt caa agt gtt gcc att ttt ggt ctt ggt gct gtt ggt tta 624
Lys Lys Gly Gln Ser Val Ala Ile Phe Gly Leu Gly Ala Val Gly Leu
          195          200          205

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sequence listing

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ggc gct gca gaa ggt gct aga atc gct ggt gct tct agg atc atc ggt 672
Gly Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly
210 215 220

gtt gat ttt aac tct aaa aga ttc gac caa gct aag gaa ttc ggt gtg 720
Val Asp Phe Asn Ser Lys Arg Phe Asp Gln Ala Lys Glu Phe Gly Val
225 230 235

acc gag tgt gtg aac ccg aaa gac cat gac aag cca att caa cag gtg 768
Thr Glu Cys Val Asn Pro Lys Asp His Asp Lys Pro Ile Gln Gln Val
245 250 255

atc gct gag atg acg gat ggt ggg gtg gac agg agt gtg gaa tgc acc 816
Ile Ala Glu Met Thr Asp Gly Gly Val Asp Arg Ser Val Glu Cys Thr
260 265 270

gga agc gtt cag gcc atg att caa gca ttt gaa tgt gtc cac gat ggc 864
Gly Ser Val Gln Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly
275 280 285

tgg ggt gtt gca gtg ctg gtg ggt gtg cca agc aaa gac gat gcc ttc 912
Trp Gly Val Ala Val Leu Val Gly Val Pro Ser Lys Asp Asp Ala Phe
290 295 300

aag act cat ccg atg aat ttc ttg aat gag agg act ctt aag ggt act 960
Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr
305 310 315

ttc ttc ggg aac tac aaa ccc aaa act gac att ccc ggg gtt gtg gaa 1008
Phe Phe Gly Asn Tyr Lys Pro Lys Thr Asp Ile Pro Gly Val Val Glu
325 330 335

aag tac atg aac aag gag ctg gag ctt gag aaa ttc atc act cac aca 1056
Lys Tyr Met Asn Lys Glu Leu Glu Leu Glu Lys Phe Ile Thr His Thr
340 345 350

gtg cca ttc tcg gaa atc aac aag gcc ttt gat tac atg ctg aag gga 1104
Val Pro Phe Ser Glu Ile Asn Lys Ala Phe Asp Tyr Met Leu Lys Gly
355 360 365

gag agt att cgt tgc atc atc acc atg ggt gct tga 1140
Glu Ser Ile Arg Cys Ile Ile Thr Met Gly Ala
370 375

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<210> 42

<211> 379

<212> PRT

<213> Arabidopsis thaliana

<400> 42

Met Ser Thr Thr Gly Gln Ile Ile Arg Cys Lys Ala Ala Val Ala Trp
1 5 10 15

Glu Ala Gly Lys Pro Leu Val Ile Glu Glu Val Glu Val Ala Pro Pro
20 25 30

Gln Lys His Glu Val Arg Ile Lys Ile Leu Phe Thr Ser Leu Cys His
35 40 45

Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Leu Phe Pro
50 55 60

sequence listing

Arg Ile Phe Gly His Glu Ala Gly Gly Ile Val Glu Ser Val Gly Glu
 65 70 75 80
 Gly Val Thr Asp Leu Gln Pro Gly Asp His Val Leu Pro Ile Phe Thr
 85 90 95
 Gly Glu Cys Gly Asp Cys Arg His Cys Gln Ser Glu Glu Ser Asn Met
 100 105 110
 Cys Asp Leu Leu Arg Ile Asn Thr Glu Arg Gly Gly Met Ile His Asp
 115 120 125
 Gly Glu Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Leu
 130 135 140
 Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Val His Ser Gly Gln Val
 145 150 155 160
 Ala Lys Ile Asn Pro Asp Ala Pro Leu Asp Lys Val Cys Ile Val Ser
 165 170 175
 Cys Gly Leu Ser Thr Gly Leu Gly Ala Thr Leu Asn Val Ala Lys Pro
 180 185 190
 Lys Lys Gly Gln Ser Val Ala Ile Phe Gly Leu Gly Ala Val Gly Leu
 195 200 205
 Gly Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly
 210 215 220
 Val Asp Phe Asn Ser Lys Arg Phe Asp Gln Ala Lys Glu Phe Gly Val
 225 230 235 240
 Thr Glu Cys Val Asn Pro Lys Asp His Asp Lys Pro Ile Gln Gln Val
 245 250 255
 Ile Ala Glu Met Thr Asp Gly Gly Val Asp Arg Ser Val Glu Cys Thr
 260 265 270
 Gly Ser Val Gln Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly
 275 280 285
 Trp Gly Val Ala Val Leu Val Gly Val Pro Ser Lys Asp Asp Ala Phe
 290 295 300
 Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr
 305 310 315 320
 Phe Phe Gly Asn Tyr Lys Pro Lys Thr Asp Ile Pro Gly Val Val Glu
 325 330 335
 Lys Tyr Met Asn Lys Glu Leu Glu Leu Glu Lys Phe Ile Thr His Thr
 340 345 350
 Val Pro Phe Ser Glu Ile Asn Lys Ala Phe Asp Tyr Met Leu Lys Gly
 355 360 365
 Glu Ser Ile Arg Cys Ile Ile Thr Met Gly Ala
 370 375

sequence listing

<211> 1140

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (1)..(1137)

<223> coding for alcohol dehydrogenase

<400> 43

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Met	Ala	Thr	Ala	Gly	Lys	Val	Ile	Lys	Cys	Lys	Ala	Ala	Val	Ala	Trp	
1				5					10					15		

gag	gcc	ggg	aag	ccg	ctg	acc	atg	gag	gag	gtg	gag	gtg	gcg	ccg	ccg	96
Glu	Ala	Gly	Lys	Pro	Leu	Thr	Met	Glu	Glu	Val	Glu	Val	Ala	Pro	Pro	
			20					25					30			

cag	gcc	atg	gag	gtg	cgc	gtc	aag	atc	ctc	ttc	acc	tcc	ctc	tgc	cac	144
Gln	Ala	Met	Glu	Val	Arg	Val	Lys	Ile	Leu	Phe	Thr	Ser	Leu	Cys	His	
		35					40					45				

acc	gac	gtc	tac	ttc	tgg	gag	gcc	aag	ggg	cag	acc	ccc	atg	ttc	cct	192
Thr	Asp	Val	Tyr	Phe	Trp	Glu	Ala	Lys	Gly	Gln	Thr	Pro	Met	Phe	Pro	
	50					55					60					

cgg	atc	ttc	ggc	cat	gaa	gct	gga	ggc	ata	gtg	gag	agt	gtt	gga	gag	240
Arg	Ile	Phe	Gly	His	Glu	Ala	Gly	Gly	Ile	Val	Glu	Ser	Val	Gly	Glu	
65					70					75					80	

ggc	gtg	act	gat	gtt	gcc	cct	ggt	gac	cac	gtc	ctc	cct	gtg	ttc	act	288
Gly	Val	Thr	Asp	Val	Ala	Pro	Gly	Asp	His	Val	Leu	Pro	Val	Phe	Thr	
				85					90					95		

ggg	gag	tgt	aag	gaa	tgc	cca	cat	tgc	aag	tct	gcg	gag	agc	aac	atg	336
Gly	Glu	Cys	Lys	Glu	Cys	Pro	His	Cys	Lys	Ser	Ala	Glu	Ser	Asn	Met	
			100					105					110			

tgt	gat	ctg	ctc	agg	atc	aac	acc	gac	aga	ggt	gtg	atg	atc	ggg	gat	384
Cys	Asp	Leu	Leu	Arg	Ile	Asn	Thr	Asp	Arg	Gly	Val	Met	Ile	Gly	Asp	
		115					120					125				

ggc	aag	tcg	cgc	ttc	tct	att	ggc	ggc	aag	ccg	att	tac	cat	ttc	gta	432
Gly	Lys	Ser	Arg	Phe	Ser	Ile	Gly	Gly	Lys	Pro	Ile	Tyr	His	Phe	Val	
	130					135					140					

ggg	act	tcc	acc	ttc	agt	gag	tac	act	gtc	atg	cat	gtc	ggt	tgt	gtt	480
Gly	Thr	Ser	Thr	Phe	Ser	Glu	Tyr	Thr	Val	Met	His	Val	Gly	Cys	Val	
145					150					155					160	

gcc	aag	atc	aac	cct	gag	gct	ccc	ctt	gat	aaa	gtc	tgt	gtt	ctt	agc	528
Ala	Lys	Ile	Asn	Pro	Glu	Ala	Pro	Leu	Asp	Lys	Val	Cys	Val	Leu	Ser	
				165					170					175		

tgt	ggt	att	tgc	act	ggt	ctt	ggc	gcg	tca	att	aat	gtt	gca	aaa	cca	576
Cys	Gly	Ile	Cys	Thr	Gly	Leu	Gly	Ala	Ser	Ile	Asn	Val	Ala	Lys	Pro	
			180					185					190			

cca	aag	ggt	tcc	aca	gtg	gcg	ata	ttt	ggg	cta	gga	gct	gtt	ggc	ctt	624
Pro	Lys	Gly	Ser	Thr	Val	Ala	Ile	Phe	Gly	Leu	Gly	Ala	Val	Gly	Leu	
		195					200					205				

gct	gct	gca	gaa	ggt	gca	agg	att	gca	ggt	gca	tca	agg	atc	att	ggt	672
Ala	Ala	Ala	Glu	Gly	Ala	Arg	Ile	Ala	Gly	Ala	Ser	Arg	Ile	Ile	Gly	

sequence listing
220

210	215	220		
gtt gac ctg aac gcc agc aga ttt gaa gag gct agg aag ttt ggc tgc Val Asp Leu Asn Ala Ser Arg Phe Glu Glu Ala Arg Lys Phe Gly Cys 225 230 235 240				720
acg gaa ttt gtg aac ccg aaa gat cac acc aag cca gtt cag cag gtg Thr Glu Phe Val Asn Pro Lys Asp His Thr Lys Pro Val Gln Gln Val 245 250 255				768
ctc gct gac atg aca aat ggc gga gtt gac cgc agt gtt gag tgc act Leu Ala Asp Met Thr Asn Gly Gly Val Asp Arg Ser Val Glu Cys Thr 260 265 270				816
ggc aac gtc aat gct atg ata caa gca ttt gaa tgt gtt cat gat ggc Gly Asn Val Asn Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly 275 280 285				864
tgg ggt gta gct gtg ctg gtg ggt gtg cca cac aag gac gct gaa ttc Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Asp Ala Glu Phe 290 295 300				912
aag acc cac ccg atg aac ttc ctg aat gag agg acc ctg aag ggc acc Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr 305 310 315 320				960
ttc ttc ggt aac ttc aag ccg cgc act gac ctg ccc aat gtc gtg gag Phe Phe Gly Asn Phe Lys Pro Arg Thr Asp Leu Pro Asn Val Val Glu 325 330 335				1008
atg tac atg aag aag gag ctg gag gtg gag aag ttc atc aca cac agc Met Tyr Met Lys Lys Glu Leu Glu Val Glu Lys Phe Ile Thr His Ser 340 345 350				1056
gtg ccg ttc tcg gag ata aac aag gcc ttc gac ctt atg gcg aag ggg Val Pro Phe Ser Glu Ile Asn Lys Ala Phe Asp Leu Met Ala Lys Gly 355 360 365				1104
gag ggc atc cgt tgc atc atc cgc atg gac aac tag Glu Gly Ile Arg Cys Ile Ile Arg Met Asp Asn 370 375				1140

<210> 44
 <211> 379
 <212> PRT
 <213> Hordeum vulgare

<400> 44
 Met Ala Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Ala Trp
 1 5 10 15
 Glu Ala Gly Lys Pro Leu Thr Met Glu Glu Val Glu Val Ala Pro Pro
 20 25 30
 Gln Ala Met Glu Val Arg Val Lys Ile Leu Phe Thr Ser Leu Cys His
 35 40 45
 Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Met Phe Pro
 50 55 60
 Arg Ile Phe Gly His Glu Ala Gly Gly Ile Val Glu Ser Val Gly Glu
 65 70 75 80

sequence listing

Gly Val Thr Asp Val Ala Pro Gly Asp His Val Leu Pro Val Phe Thr
 85 90 95
 Gly Glu Cys Lys Glu Cys Pro His Cys Lys Ser Ala Glu Ser Asn Met
 100 105 110
 Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Gly Asp
 115 120 125
 Gly Lys Ser Arg Phe Ser Ile Gly Gly Lys Pro Ile Tyr His Phe Val
 130 135 140
 Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Met His Val Gly Cys Val
 145 150 155 160
 Ala Lys Ile Asn Pro Glu Ala Pro Leu Asp Lys Val Cys Val Leu Ser
 165 170 175
 Cys Gly Ile Cys Thr Gly Leu Gly Ala Ser Ile Asn Val Ala Lys Pro
 180 185 190
 Pro Lys Gly Ser Thr Val Ala Ile Phe Gly Leu Gly Ala Val Gly Leu
 195 200 205
 Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly
 210 215 220
 Val Asp Leu Asn Ala Ser Arg Phe Glu Glu Ala Arg Lys Phe Gly Cys
 225 230 235 240
 Thr Glu Phe Val Asn Pro Lys Asp His Thr Lys Pro Val Gln Gln Val
 245 250 255
 Leu Ala Asp Met Thr Asn Gly Gly Val Asp Arg Ser Val Glu Cys Thr
 260 265 270
 Gly Asn Val Asn Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly
 275 280 285
 Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Asp Ala Glu Phe
 290 295 300
 Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr
 305 310 315 320
 Phe Phe Gly Asn Phe Lys Pro Arg Thr Asp Leu Pro Asn Val Val Glu
 325 330 335
 Met Tyr Met Lys Lys Glu Leu Glu Val Glu Lys Phe Ile Thr His Ser
 340 345 350
 Val Pro Phe Ser Glu Ile Asn Lys Ala Phe Asp Leu Met Ala Lys Gly
 355 360 365
 Glu Gly Ile Arg Cys Ile Ile Arg Met Asp Asn
 370 375

<210> 45
 <211> 1140
 <212> DNA
 <213> Oryza sativa

sequence listing

<220>

<221> CDS

<222> (1)..(1137)

<223> coding for alcohol dehydrogenase

<400> 45

atg gcg acc gca ggg aag gtg atc aag tgc aaa gcg gcg gtg gca tgg	48
Met Ala Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Ala Trp	
1 5 10 15	
gag gcc gcg aag ccg ctg gtg atc gag gag gtg gag gtg gcg ccg ccg	96
Glu Ala Ala Lys Pro Leu Val Ile Glu Glu Val Glu Val Ala Pro Pro	
20 25 30	
cag gcc atg gag gtg cgc gtc aag atc ctc ttc acc tcg ctc tgc cac	144
Gln Ala Met Glu Val Arg Val Lys Ile Leu Phe Thr Ser Leu Cys His	
35 40 45	
acc gac gtc tac ttc tgg gag gcc aag gga cag act ccc gtg ttc cct	192
Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Val Phe Pro	
50 55 60	
cgg atc ttc ggc cat gaa gct gga ggt att gtg gag agt gtt gga gag	240
Arg Ile Phe Gly His Glu Ala Gly Gly Ile Val Glu Ser Val Gly Glu	
65 70 75 80	
ggt gtg act gat ctt gcc cct ggt gac cat gtt ctc cct gtg ttc act	288
Gly Val Thr Asp Leu Ala Pro Gly Asp His Val Leu Pro Val Phe Thr	
85 90 95	
ggg gag tgc aag gag tgt gcc cac tgc aag tca gca gag agc aac atg	336
Gly Glu Cys Lys Glu Cys Ala His Cys Lys Ser Ala Glu Ser Asn Met	
100 105 110	
tgt gat ctg ctc agg atc aac act gac agg ggt gtg atg att ggt gat	384
Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Gly Asp	
115 120 125	
ggc aaa tca cgc ttt tcc atc aac ggg aag ccc att tac cat ttc gtc	432
Gly Lys Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Val	
130 135 140	
ggg act tcg acc ttc agc gag tac act gtc atg cat gtt ggt tgc gtt	480
Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Met His Val Gly Cys Val	
145 150 155 160	
gcg aag atc aac ccg gca gct cca ctt gat aaa gtt tgc gtt ctt agc	528
Ala Lys Ile Asn Pro Ala Ala Pro Leu Asp Lys Val Cys Val Leu Ser	
165 170 175	
tgt ggt att tct act ggt ctt ggt gct aca atc aat gtg gca aag cca	576
Cys Gly Ile Ser Thr Gly Leu Gly Ala Thr Ile Asn Val Ala Lys Pro	
180 185 190	
cca aag ggt tcg acg gtg gcg ata ttt ggt cta gga gct gta ggc ctt	624
Pro Lys Gly Ser Thr Val Ala Ile Phe Gly Leu Gly Ala Val Gly Leu	
195 200 205	
gct gcc gca gaa ggt gca agg att gca gga gcg tca agg atc att ggc	672
Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly	
210 215 220	
att gac ctg aac gcc aac aga ttt gaa gaa gct agg aaa ttt ggt tgc	720

sequence listing

Ile 225	Asp	Leu	Asn	Ala	Asn 230	Arg	Phe	Glu	Glu	Ala 235	Arg	Lys	Phe	Gly	Cys 240	
act	gaa	ttt	gtg	aac	cca	aag	gac	cat	gac	aag	cca	ggt	cag	cag	gta	768
Thr	Glu	Phe	Val	Asn 245	Pro	Lys	Asp	His	Asp 250	Lys	Pro	Val	Gln	Gln	Val 255	
ctt	gct	gag	atg	acc	aat	ggc	gga	gtt	gac	cgc	agc	ggt	gaa	tgc	act	816
Leu	Ala	Glu	Met 260	Thr	Asn	Gly	Gly	Val 265	Asp	Arg	Ser	Val	Glu 270	Cys	Thr	
ggc	aac	atc	aac	gcc	atg	atc	caa	gca	ttt	gaa	tgt	gtt	cat	gat	ggc	864
Gly	Asn 275	Ile	Asn	Ala	Met	Ile	Gln 280	Ala	Phe	Glu	Cys	Val 285	His	Asp	Gly	
tgg	ggt	gtt	gct	gtt	ttg	gtc	ggc	gtg	cca	cac	aag	gac	gcc	gag	ttc	912
Trp	Gly 290	Val	Ala	Val	Leu	Val 295	Gly	Val	Pro	His	Lys 300	Asp	Ala	Glu	Phe	
aag	acc	cac	ccg	atg	aac	ttc	ctg	aac	gag	agg	act	ctc	aag	gga	acc	960
Lys 305	Thr	His	Pro	Met	Asn 310	Phe	Leu	Asn	Glu	Arg 315	Thr	Leu	Lys	Gly	Thr 320	
ttc	ttc	ggc	aac	tac	aag	cca	cgc	acc	gat	ctg	ccc	aac	gtc	gtc	gag	1008
Phe	Phe	Gly	Asn 325	Tyr	Lys	Pro	Arg	Thr	Asp 330	Leu	Pro	Asn	Val	Val 335	Glu	
ctc	tac	atg	aag	aag	gag	ctg	gag	gtg	gag	aag	ttc	atc	aca	cac	agc	1056
Leu	Tyr	Met 340	Lys	Lys	Glu	Leu	Glu	Val 345	Glu	Lys	Phe	Ile	Thr 350	His	Ser	
gtg	ccg	ttc	tcg	gag	atc	aac	acg	gcg	ttc	gac	ctg	atg	cac	aag	ggc	1104
Val	Pro 355	Phe	Ser	Glu	Ile	Asn	Thr 360	Ala	Phe	Asp	Leu	Met 365	His	Lys	Gly	
gag	ggc	atc	cgc	tgc	atc	atc	cgc	atg	gag	aac	tga					1140
Glu 370	Gly	Ile	Arg	Cys	Ile 375	Ile	Arg	Met	Glu	Asn						

<210> 46

<211> 379

<212> PRT

<213> Oryza sativa

<400> 46

Met Ala Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Ala Trp
1 5 10 15

Glu Ala Ala Lys Pro Leu Val Ile Glu Glu Val Glu Val Ala Pro Pro
20 25 30

Gln Ala Met Glu Val Arg Val Lys Ile Leu Phe Thr Ser Leu Cys His
35 40 45

Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Val Phe Pro
50 55 60

Arg Ile Phe Gly His Glu Ala Gly Gly Ile Val Glu Ser Val Gly Glu
65 70 75 80

Gly Val Thr Asp Leu Ala Pro Gly Asp His Val Leu Pro Val Phe Thr
85 90 95

sequence listing

Gly Glu Cys Lys Glu Cys Ala His Cys Lys Ser Ala Glu Ser Asn Met
 100 105 110
 Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Gly Asp
 115 120 125
 Gly Lys Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Val
 130 135 140
 Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Met His Val Gly Cys Val
 145 150 155 160
 Ala Lys Ile Asn Pro Ala Ala Pro Leu Asp Lys Val Cys Val Leu Ser
 165 170 175
 Cys Gly Ile Ser Thr Gly Leu Gly Ala Thr Ile Asn Val Ala Lys Pro
 180 185 190
 Pro Lys Gly Ser Thr Val Ala Ile Phe Gly Leu Gly Ala Val Gly Leu
 195 200 205
 Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly
 210 215 220
 Ile Asp Leu Asn Ala Asn Arg Phe Glu Glu Ala Arg Lys Phe Gly Cys
 225 230 235 240
 Thr Glu Phe Val Asn Pro Lys Asp His Asp Lys Pro Val Gln Gln Val
 245 250 255
 Leu Ala Glu Met Thr Asn Gly Gly Val Asp Arg Ser Val Glu Cys Thr
 260 265 270
 Gly Asn Ile Asn Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly
 275 280 285
 Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Asp Ala Glu Phe
 290 295 300
 Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr
 305 310 315 320
 Phe Phe Gly Asn Tyr Lys Pro Arg Thr Asp Leu Pro Asn Val Val Glu
 325 330 335
 Leu Tyr Met Lys Lys Glu Leu Glu Val Glu Lys Phe Ile Thr His Ser
 340 345 350
 Val Pro Phe Ser Glu Ile Asn Thr Ala Phe Asp Leu Met His Lys Gly
 355 360 365
 Glu Gly Ile Arg Cys Ile Ile Arg Met Glu Asn
 370 375

<210> 47
 <211> 1140
 <212> DNA
 <213> Zea mays
 <220>
 <221> CDS
 <222> (1)..(1137)

sequence listing

<223> coding for alcohol dehydrogenase

<400> 47

atg gcg acc gcg ggg aag gtg atc aag tgc aaa gct gcg gtg gca tgg	48
Met Ala Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Ala Trp	
1 5 10 15	
gag gcc ggc aag cca ctg tcg atc gag gag gtg gag gta gcg cct ccg	96
Glu Ala Gly Lys Pro Leu Ser Ile Glu Glu Val Glu Val Ala Pro Pro	
20 25 30	
cag gcc atg gag gtg cgc gtc aag atc ctc ttc acc tcg ctc tgc cac	144
Gln Ala Met Glu Val Arg Val Lys Ile Leu Phe Thr Ser Leu Cys His	
35 40 45	
acc gac gtc tac ttc tgg gag gcc aag ggg cag act ccc gtg ttc cct	192
Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Val Phe Pro	
50 55 60	
cgg atc ttt ggc cat gag gct gga ggt atc ata gag agt gtt gga gag	240
Arg Ile Phe Gly His Glu Ala Gly Gly Ile Ile Glu Ser Val Gly Glu	
65 70 75 80	
ggt gtg act gac gta gct ccg ggc gac cat gtc ctt cct gtg ttc act	288
Gly Val Thr Asp Val Ala Pro Gly Asp His Val Leu Pro Val Phe Thr	
85 90 95	
ggg gag tgc aag gag tgc gcc cac tgc aag tcg gca gag agc aac atg	336
Gly Glu Cys Lys Glu Cys Ala His Cys Lys Ser Ala Glu Ser Asn Met	
100 105 110	
tgt gat ttg ctc agg atc aac act gac cgc ggt gtg atg att ggc gat	384
Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Gly Asp	
115 120 125	
ggc aag tcg cgg ttt tca atc aat ggg aag cct atc tac cac ttt gtt	432
Gly Lys Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Val	
130 135 140	
ggg act tcc acc ttc agc gag tac acc gtc atg cat gtc ggt tgt gtt	480
Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Met His Val Gly Cys Val	
145 150 155 160	
gca aag atc aac cct cag gct ccc ctt gat aaa gtt tgc gtc ctt agc	528
Ala Lys Ile Asn Pro Gln Ala Pro Leu Asp Lys Val Cys Val Leu Ser	
165 170 175	
tgt ggt att tct act ggt ctt ggt gca tca att aat gtt gca aaa cct	576
Cys Gly Ile Ser Thr Gly Leu Gly Ala Ser Ile Asn Val Ala Lys Pro	
180 185 190	
ccg aag ggt tcg aca gtg gct gtt ttc ggt tta gga gcc gtt ggt ctt	624
Pro Lys Gly Ser Thr Val Ala Val Phe Gly Leu Gly Ala Val Gly Leu	
195 200 205	
gcc gct gca gaa ggt gca agg att gct gga gcg tca agg atc att ggt	672
Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly	
210 215 220	
gtc gac ctg aac ccc agc aga ttc gaa gaa gct agg aag ttc ggt tgc	720
Val Asp Leu Asn Pro Ser Arg Phe Glu Glu Ala Arg Lys Phe Gly Cys	
225 230 235 240	

sequence listing

act gaa ttt gtg aac cca aaa gac cac aac aag ccg gtg cag gag gta	768
Thr Glu Phe Val Asn Pro Lys Asp His Asn Lys Pro Val Gln Glu Val	
245 250 255	
ctt gct gag atg acc aac gga ggg gtc gac cgc agc gtg gaa tgc act	816
Leu Ala Glu Met Thr Asn Gly Gly Val Asp Arg Ser Val Glu Cys Thr	
260 265 270	
ggc aac atc aat gct atg atc caa gct ttc gaa tgt gtt cat gat ggc	864
Gly Asn Ile Asn Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly	
275 280 285	
tgg ggt gtt gcc gtg ctg gtg ggt gtg ccg cat aag gac gct gag ttc	912
Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Asp Ala Glu Phe	
290 295 300	
aag acc cac ccg atg aac ttc ctg aac gaa agg acc ctg aag ggg acc	960
Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr	
305 310 315 320	
ttc ttt ggc aac tat aag cca cgc act gat ctg cca aat gtg gtg gag	1008
Phe Phe Gly Asn Tyr Lys Pro Arg Thr Asp Leu Pro Asn Val Val Glu	
325 330 335	
ctg tac atg aaa aag gag ctg gag gtg gag aag ttc atc acg cac agc	1056
Leu Tyr Met Lys Lys Glu Leu Glu Val Glu Lys Phe Ile Thr His Ser	
340 345 350	
gtc ccg ttc gcg gag atc aac aag gcg ttc aac ctg atg gcc aag ggg	1104
Val Pro Phe Ala Glu Ile Asn Lys Ala Phe Asn Leu Met Ala Lys Gly	
355 360 365	
gag ggc atc cgc tgc atc atc cgc atg gag aac tag	1140
Glu Gly Ile Arg Cys Ile Ile Arg Met Glu Asn	
370 375	

<210> 48

<211> 379

<212> PRT

<213> Zea mays

<400> 48

Met Ala Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Ala Trp

1

5

10

15

Glu Ala Gly Lys Pro Leu Ser Ile Glu Glu Val Glu Val Ala Pro Pro

20

25

30

Gln Ala Met Glu Val Arg Val Lys Ile Leu Phe Thr Ser Leu Cys His

35

40

45

Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Val Phe Pro

50

55

60

Arg Ile Phe Gly His Glu Ala Gly Gly Ile Ile Glu Ser Val Gly Glu

65

70

75

80

Gly Val Thr Asp Val Ala Pro Gly Asp His Val Leu Pro Val Phe Thr

85

90

95

Gly Glu Cys Lys Glu Cys Ala His Cys Lys Ser Ala Glu Ser Asn Met

100

105

110

sequence listing

Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Gly Asp
115 120 125

Gly Lys Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Val
130 135 140

Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Met His Val Gly Cys Val
145 150 155 160

Ala Lys Ile Asn Pro Gln Ala Pro Leu Asp Lys Val Cys Val Leu Ser
165 170 175

Cys Gly Ile Ser Thr Gly Leu Gly Ala Ser Ile Asn Val Ala Lys Pro
180 185 190

Pro Lys Gly Ser Thr Val Ala Val Phe Gly Leu Gly Ala Val Gly Leu
195 200 205

Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly
210 215 220

Val Asp Leu Asn Pro Ser Arg Phe Glu Glu Ala Arg Lys Phe Gly Cys
225 230 235 240

Thr Glu Phe Val Asn Pro Lys Asp His Asn Lys Pro Val Gln Glu Val
245 250 255

Leu Ala Glu Met Thr Asn Gly Gly Val Asp Arg Ser Val Glu Cys Thr
260 265 270

Gly Asn Ile Asn Ala Met Ile Gln Ala Phe Glu Cys Val His Asp Gly
275 280 285

Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Asp Ala Glu Phe
290 295 300

Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly Thr
305 310 315 320

Phe Phe Gly Asn Tyr Lys Pro Arg Thr Asp Leu Pro Asn Val Val Glu
325 330 335

Leu Tyr Met Lys Lys Glu Leu Glu Val Glu Lys Phe Ile Thr His Ser
340 345 350

Val Pro Phe Ala Glu Ile Asn Lys Ala Phe Asn Leu Met Ala Lys Gly
355 360 365

Glu Gly Ile Arg Cys Ile Ile Arg Met Glu Asn
370 375

<210> 49

<211> 505

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
sense RNA-fragment of E.coli codA gene

<400> 49

aagcttggt aacagtgtcg aataacgctt tacaacaat tattaacgcc cggttaccag 60
gcgaagaggg gctgtggcag attcatctgc aggacgaaa aatcagcgcc attgatgcgc 120

sequence listing

```

aatccggcgt gatgccata actgaaaaca gcctggatgc cgaacaaggt ttagttatac 180
cgccgtttgt ggagccacat attcacctgg acaccacgca aaccgccgga caaccgaact 240
ggaatcagtc cggcacgctg tttgaaggca ttgaacgctg ggccgagcgc aaagcggtat 300
taacccatga cgatgtgaaa caacgcgcgc ggcaaacgct gaaatggcag attgccaacg 360
gcattcagca tgtgcgtacc catgtcgatg tttcggatgc aacgctaact gcgctgaaag 420
caatgctgga agtgaagcag gaagtcgcgc cgtggattga tctgcaaadc gtcgccttcc 480
ctcaggaagg gattttgtcg tcgac                                     505

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<210> 50
 <211> 27
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 50
 cgtaatacgc gcgtggagtc g 21

<210> 51
 <211> 26
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 51
 cggcaggata atcaggttgg 20

<210> 52
 <211> 505
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence: coding for
 antisense RNA-fragment of E.coli codA gene

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<400> 52
gaattcggct aacagtgtcg aataacgctt tacaaacaat tattaacgcc cggttaccag 60
gcgaagaggg gctgtggcag attcatctgc aggacggaaa aatcagcgcc attgatgcgc 120
aatccggcgt gatgccata actgaaaaca gcctggatgc cgaacaaggt ttagttatac 180
cgccgtttgt ggagccacat attcacctgg acaccacgca aaccgccgga caaccgaact 240
ggaatcagtc cggcacgctg tttgaaggca ttgaacgctg ggccgagcgc aaagcggtat 300
taacccatga cgatgtgaaa caacgcgcgc ggcaaacgct gaaatggcag attgccaacg 360
gcattcagca tgtgcgtacc catgtcgatg tttcggatgc aacgctaact gcgctgaaag 420
caatgctgga agtgaagcag gaagtcgcgc cgtggattga tctgcaaadc gtcgccttcc 480
ctcaggaagg gattttgtcg gatcc                                     505

```

<210> 53
 <211> 27
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 53
 gtcaacgtaa ccaaccctgc 20

sequence listing

<210> 54
 <211> 26
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 54
 ggatccgaca aaatcccttc ctgagg

26

<210> 55
 <211> 5674
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence: vector
 construct pBluKS-nitP-STLS1-35S-T

<400> 55
 ccagcttttg ttcccttttag tgaggggttaa tttcgagctt ggcgtaatca tggatcatagc 60
 tgtttcctgt gtgaaattgt tatccgctca caattccaca caacatacga gccggaagca 120
 taaagtgtaa agcctggggg gcctaattgag tgagctaact cacattaatt gcgttgcgct 180
 cactgccccg tttccagtcg ggaaacctgt cgtgccagct gcattaatga atcggccaac 240
 gcgcggggag aggcggtttg cgtattgggc gctcttccgc ttctcgcgc actgactcgc 300
 tgcgctcggg cgttcggctg cggcgagcgg tatcagctca ctcaaaggcg gtaatacggg 360
 tatccacaga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc cagcaaaagg 420
 ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc cccctgacg 480
 agcatcaca aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga ctataaagat 540
 accaggcggt tccccctgga agctccctcg tgcgctctcc tgttccgacc ctgcccgtta 600
 ccggatacct gtccgccttt ctcccttcgg gaagcgtggc gctttctcat agctcacgct 660
 gtaggtatct cagttcgggtg taggtcgttc gctccaagct gggctgtgtg cacgaacccc 720
 ccgttcagcc cgaccgctgc gccttatccg gtaactatcg tcttgagtcc aaccgggtaa 780
 gacacgactt atcgccactg gcagcagcca ctggttaacag gattagcaga gcgaggtatg 840
 taggcgtgct tacagagttc ttgaagtggg ggcctaacta cggctacact agaaggacag 900
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<211> 6046

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: binary vector pSUN1

sequence listing

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sequence listing

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<211> 9838

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Transgenic expression vector for codA dsRNA pSUN1-codA-RNAi

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sequence listing

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		130				135				140							
ccc	ccg	cac	atc	atc	ctc	cgc	aag	ggc	ctc	gtc	gcc	ggt	gtc	gag	tac	480	
Pro	Pro	His	Ile	Ile	Leu	Arg	Lys	Gly	Leu	Val	Ala	Gly	Val	Glu	Tyr		
145					150					155				160			
ccg	ctg	ctc	gcc	gac	cac	atg	tcc	gat	tac	atg	gcc	aag	acg	ctc	ttc	528	
Pro	Leu	Leu	Ala	Asp	His	Met	Ser	Asp	Tyr	Met	Ala	Lys	Thr	Leu	Phe		
				165					170					175			
ttc	acc	tcc	ctc	ctc	tat	aac	aat	acc	acg	gat	cat	aag	aac	gga	gtt	576	
Phe	Thr	Ser	Leu	Leu	Tyr	Asn	Asn	Thr	Thr	Asp	His	Lys	Asn	Gly	Val		
			180					185					190				
gct	aag	tac	tct	gcg	aac	gtg	gag	atg	tgt	agg	ctc	acg	gag	caa	gtt	624	
Ala	Lys	Tyr	Ser	Ala	Asn	Val	Glu	Met	Cys	Arg	Leu	Thr	Glu	Gln	Val		
		195				200						205					
gtg	ttc	tcg	gac	cca	tac	cgt	gtt	tcc	aaa	ttt	aat	cgg	tgg	acc	tcg	672	
Val	Phe	Ser	Asp	Pro	Tyr	Arg	Val	Ser	Lys	Phe	Asn	Arg	Trp	Thr	Ser		
		210				215					220						
cct	tat	ctc	gac	aaa	gat	gct	gag	gca	gtt	cgc	gag	gat	gat	gag	ctc	720	
Pro	Tyr	Leu	Asp	Lys	Asp	Ala	Glu	Ala	Val	Arg	Glu	Asp	Asp	Glu	Leu		
225					230					235				240			
aag	ttg	gaa	gta	gct	ggg	ctg	aaa	tcg	atg	ttt	atc	gag	aga	gct	caa	768	
Lys	Leu	Glu	Val	Ala	Gly	Leu	Lys	Ser	Met	Phe	Ile	Glu	Arg	Ala	Gln		
				245				250						255			
gct	ctg	att	cat	gga	gat	ctc	cac	act	ggt	tct	atc	atg	gtg	acc	gaa	816	
Ala	Leu	Ile	His	Gly	Asp	Leu	His	Thr	Gly	Ser	Ile	Met	Val	Thr	Glu		
			260					265					270				
gtt	caa	ctc	aag	tca	ttg	atc	cag	aat	ttg	ggt	tct	atg	ggg	cca	atg	864	
Val	Gln	Leu	Lys	Ser	Leu	Ile	Gln	Asn	Leu	Gly	Ser	Met	Gly	Pro	Met		
		275					280					285					
ggg	ttt	gat	att	ggg	agc	ctt	cct	tgg	aaa	cct	gat	ttt	ggg	cat	act	912	
Gly	Phe	Asp	Ile	Gly	Ser	Leu	Pro	Trp	Lys	Pro	Asp	Phe	Gly	His	Thr		
		290				295				300							
atg	cac	aga	atg	ggc	atg	ctg	atc	aag	cga	atg	atc	gta	agg	ctt	aca	960	
Met	His	Arg	Met	Gly	Met	Leu	Ile	Lys	Arg	Met	Ile	Val	Arg	Leu	Thr		
305					310					315				320			
aga	atg	gat	ctt	gaa	gac	aat	tgaagagtcg	tggaattt	gtg	tccacaaaaa						1011	
Arg	Met	Asp	Leu	Glu	Asp	Asn				325							

<210> 60
 <211> 327
 <212> PRT
 <213> Zea mays

<400> 60
 Ala Arg Ala Leu Leu Ser Ser Pro Leu Ala Gly Ala Ser Pro Asp Cys
 1 5 10 15

sequence listing

Gln Ser Ala Ser Ala Met Ala Ala Glu Glu Glu Gln Gly Phe Arg Pro
20 25 30
Leu Asp Glu Ser Ser Leu Leu Ala Tyr Ile Lys Ala Thr Pro Ala Leu
35 40 45
Ala Ser Arg Leu Gly Gly Gly Gly Ser Leu Asp Ser Ile Glu Ile Lys
50 55 60
Glu Val Gly Asp Gly Asn Leu Asn Phe Val Tyr Ile Val Gln Ser Glu
65 70 75 80
Ala Gly Ala Ile Val Val Lys Gln Ala Leu Pro Tyr Val Arg Cys Val
85 90 95
Gly Asp Ser Trp Pro Met Thr Arg Glu Arg Ala Tyr Phe Glu Ala Ser
100 105 110
Thr Leu Arg Glu His Gly Arg Leu Cys Pro Glu His Thr Pro Glu Val
115 120 125
Tyr His Phe Asp Arg Thr Leu Ser Leu Met Gly Met Arg Tyr Ile Glu
130 135 140
Pro Pro His Ile Ile Leu Arg Lys Gly Leu Val Ala Gly Val Glu Tyr
145 150 155 160
Pro Leu Leu Ala Asp His Met Ser Asp Tyr Met Ala Lys Thr Leu Phe
165 170 175
Phe Thr Ser Leu Leu Tyr Asn Asn Thr Thr Asp His Lys Asn Gly Val
180 185 190
Ala Lys Tyr Ser Ala Asn Val Glu Met Cys Arg Leu Thr Glu Gln Val
195 200 205
Val Phe Ser Asp Pro Tyr Arg Val Ser Lys Phe Asn Arg Trp Thr Ser
210 215 220
Pro Tyr Leu Asp Lys Asp Ala Glu Ala Val Arg Glu Asp Asp Glu Leu
225 230 235 240
Lys Leu Glu Val Ala Gly Leu Lys Ser Met Phe Ile Glu Arg Ala Gln
245 250 255
Ala Leu Ile His Gly Asp Leu His Thr Gly Ser Ile Met Val Thr Glu
260 265 270
Val Gln Leu Lys Ser Leu Ile Gln Asn Leu Gly Ser Met Gly Pro Met
275 280 285
Gly Phe Asp Ile Gly Ser Leu Pro Trp Lys Pro Asp Phe Gly His Thr
290 295 300
Met His Arg Met Gly Met Leu Ile Lys Arg Met Ile Val Arg Leu Thr
305 310 315 320
Arg Met Asp Leu Glu Asp Asn
325

<210> 61
<211> 471

sequence listing

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (2)..(469)

<223> coding for 5-methylthioribose kinase

<400> 61

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a ttt ccg ggt cga cga ttt cgt ggc aat ctc aac ttc gtt ttc atc gtc 49
  Phe Pro Gly Arg Arg Phe Arg Gly Asn Leu Asn Phe Val Phe Ile Val
    1             5             10             15

atc gga tcc act ggc tca ctc gtc atc aaa cag gcg ctt ccg tat ata 97
Ile Gly Ser Thr Gly Ser Leu Val Ile Lys Gln Ala Leu Pro Tyr Ile
                20             25             30

cgt tgt att ggg gag tct tgg cca atg acg aaa gaa aga gct tac ttt 145
Arg Cys Ile Gly Glu Ser Trp Pro Met Thr Lys Glu Arg Ala Tyr Phe
                35             40             45

gaa gct aca act ctg aga aag cac gga gct ttg tct cct gat cat gtt 193
Glu Ala Thr Thr Leu Arg Lys His Gly Ala Leu Ser Pro Asp His Val
                50             55             60

cct gaa gtc tac cat ttt gac agg acc atg gct ttg att gga atg agg 241
Pro Glu Val Tyr His Phe Asp Arg Thr Met Ala Leu Ile Gly Met Arg
                65             70             75             80

tat ctg gag cct cct cac atc atc ctc cgc aaa gga ctc gtt gct gga 289
Tyr Leu Glu Pro Pro His Ile Ile Leu Arg Lys Gly Leu Val Ala Gly
                85             90             95

atc cag tac cct ttc ctt gca gaa cac atg gct gat tac atg gcc aaa 337
Ile Gln Tyr Pro Phe Leu Ala Glu His Met Ala Asp Tyr Met Ala Lys
                100             105             110

acc ctc ttc ttc act tcg ctc ctc tat cat gat acc aca gag cac aaa 385
Thr Leu Phe Phe Thr Ser Leu Leu Tyr His Asp Thr Thr Glu His Lys
                115             120             125

aga gca gta acc gag ttt tgt ggt aat gtg gag tta tgc cgg tta acg 433
Arg Ala Val Thr Glu Phe Cys Gly Asn Val Glu Leu Cys Arg Leu Thr
                130             135             140

gag caa gta gtg ttc tct gac ccg tat aga gtt tct ag 471
Glu Gln Val Val Phe Ser Asp Pro Tyr Arg Val Ser
145             150             155

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<210> 62

<211> 156

<212> PRT

<213> Brassica napus

<400> 62

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Phe Pro Gly Arg Arg Phe Arg Gly Asn Leu Asn Phe Val Phe Ile Val
  1             5             10             15

Ile Gly Ser Thr Gly Ser Leu Val Ile Lys Gln Ala Leu Pro Tyr Ile
    20             25             30

Arg Cys Ile Gly Glu Ser Trp Pro Met Thr Lys Glu Arg Ala Tyr Phe
    35             40             45

```

sequence listing

Glu Ala Thr Thr Leu Arg Lys His Gly Ala Leu Ser Pro Asp His Val
50 55 60
Pro Glu Val Tyr His Phe Asp Arg Thr Met Ala Leu Ile Gly Met Arg
65 70 75 80
Tyr Leu Glu Pro Pro His Ile Ile Leu Arg Lys Gly Leu Val Ala Gly
85 90 95
Ile Gln Tyr Pro Phe Leu Ala Glu His Met Ala Asp Tyr Met Ala Lys
100 105 110
Thr Leu Phe Phe Thr Ser Leu Leu Tyr His Asp Thr Thr Glu His Lys
115 120 125
Arg Ala Val Thr Glu Phe Cys Gly Asn Val Glu Leu Cys Arg Leu Thr
130 135 140
Glu Gln Val Val Phe Ser Asp Pro Tyr Arg Val Ser
145 150 155

<210> 63
<211> 415
<212> DNA
<213> Brassica napus
<220>
<221> CDS
<222> (3)..(413)
<223> coding for 5-methylthioribose kinase

<400> 63
gg gtc gac gat ttc gtg ctg aga gca aaa gag atg tcg ttc gat gag 47
Val Asp Asp Phe Val Leu Arg Ala Lys Glu Met Ser Phe Asp Glu
1 5 10 15
ttc aag ccg ttg aac gag aaa tct cta gta gag tac ata aag gca acg 95
Phe Lys Pro Leu Asn Glu Lys Ser Leu Val Glu Tyr Ile Lys Ala Thr
20 25 30
cct gcc ctc tcc tcc agg ctc gga gac aag tac gat gat ctg gtc atc 143
Pro Ala Leu Ser Ser Arg Leu Gly Asp Lys Tyr Asp Asp Leu Val Ile
35 40 45
aag gaa gtt gga gat ggc aat ctc aac ttc gtt ttc atc gtt gtc gga 191
Lys Glu Val Gly Asp Gly Asn Leu Asn Phe Val Phe Ile Val Val Gly
50 55 60
tcc act ggc tca ctc gtc atc aaa cag gcg ctt ccg tat ata cgt tgt 239
Ser Thr Gly Ser Leu Val Ile Lys Gln Ala Leu Pro Tyr Ile Arg Cys
65 70 75
att gga gaa tca tgg cca atg acg aaa gaa aga gct tac ttt gaa gca 287
Ile Gly Glu Ser Trp Pro Met Thr Lys Glu Arg Ala Tyr Phe Glu Ala
80 85 90 95
aca act ctg aga aag cac ggt ggt ttg tct ccg gat cat gtt cct gaa 335
Thr Thr Leu Arg Lys His Gly Gly Leu Ser Pro Asp His Val Pro Glu
100 105 110
gtc tac cat ttt gac aga acc atg gct ttg att gga atg aga tac ctc 383
Val Tyr His Phe Asp Arg Thr Met Ala Leu Ile Gly Met Arg Tyr Leu

sequence listing

115 120 125 415

gag cct cct cac atc atc ctc cgc aaa gga ct
 Glu Pro Pro His Ile Ile Leu Arg Lys Gly
 130 135

<210> 64
 <211> 137
 <212> PRT
 <213> Brassica napus

<400> 64
 Val Asp Asp Phe Val Leu Arg Ala Lys Glu Met Ser Phe Asp Glu Phe
 1 5 10 15
 Lys Pro Leu Asn Glu Lys Ser Leu Val Glu Tyr Ile Lys Ala Thr Pro
 20 25 30
 Ala Leu Ser Ser Arg Leu Gly Asp Lys Tyr Asp Asp Leu Val Ile Lys
 35 40 45
 Glu Val Gly Asp Gly Asn Leu Asn Phe Val Phe Ile Val Val Gly Ser
 50 55 60
 Thr Gly Ser Leu Val Ile Lys Gln Ala Leu Pro Tyr Ile Arg Cys Ile
 65 70 75 80
 Gly Glu Ser Trp Pro Met Thr Lys Glu Arg Ala Tyr Phe Glu Ala Thr
 85 90 95
 Thr Leu Arg Lys His Gly Gly Leu Ser Pro Asp His Val Pro Glu Val
 100 105 110
 Tyr His Phe Asp Arg Thr Met Ala Leu Ile Gly Met Arg Tyr Leu Glu
 115 120 125
 Pro Pro His Ile Ile Leu Arg Lys Gly
 130 135

<210> 65
 <211> 424
 <212> DNA
 <213> Oryza sativa
 <220>
 <221> CDS
 <222> (3)..(422)
 <223> coding for 5-methylthioribose kinase

<400> 65
 cc ctt ctc tac aac tcc acc act gat cac aag aaa gga gtt gct cag 47
 Leu Leu Tyr Asn Ser Thr Thr Asp His Lys Lys Gly Val Ala Gln
 1 5 10 15
 tac tgc gat aat gtg gag atg tgt agg ctc aca gag caa gtc gtg ttc 95
 Tyr Cys Asp Asn Val Glu Met Cys Arg Leu Thr Glu Gln Val Val Phe
 20 25 30
 tca gac cca tac atg ctc gcc aaa tac aat cgt tgc aca tca ccc ttc 143
 Ser Asp Pro Tyr Met Leu Ala Lys Tyr Asn Arg Cys Thr Ser Pro Phe
 35 40 45

sequence listing

cta gat aat gat gct gca gcg gtt cga gag gat gct gag ctt aaa ttg	191
Leu Asp Asn Asp Ala Ala Ala Val Arg Glu Asp Ala Glu Leu Lys Leu	
50 55 60	
gag att gct gaa ttg aaa tca atg ttt att gag aga gca cag gct ctt	239
Glu Ile Ala Glu Leu Lys Ser Met Phe Ile Glu Arg Ala Gln Ala Leu	
65 70 75	
ctt cat gga gat ctc cac act ggt tcc atc atg gtg aca cca gat tct	287
Leu His Gly Asp Leu His Thr Gly Ser Ile Met Val Thr Pro Asp Ser	
80 85 90 95	
act caa gtg att gat cca gaa ttt gct ttc tat ggc cca atg ggt tac	335
Thr Gln Val Ile Asp Pro Glu Phe Ala Phe Tyr Gly Pro Met Gly Tyr	
100 105 110	
gac att ggg gcc ttc ctg ggg aac ttg att ttg gca tat ttt tca caa	383
Asp Ile Gly Ala Phe Leu Gly Asn Leu Ile Leu Ala Tyr Phe Ser Gln	
115 120 125	
gat gga cac gct gat caa gca aat gat cgt aag gct tac aa	424
Asp Gly His Ala Asp Gln Ala Asn Asp Arg Lys Ala Tyr	
130 135 140	

<210> 66
 <211> 140
 <212> PRT
 <213> Oryza sativa

<400> 66

Leu Leu Tyr Asn Ser Thr Thr Asp His Lys Lys Gly Val Ala Gln Tyr	
1 5 10 15	
Cys Asp Asn Val Glu Met Cys Arg Leu Thr Glu Gln Val Val Phe Ser	
20 25 30	
Asp Pro Tyr Met Leu Ala Lys Tyr Asn Arg Cys Thr Ser Pro Phe Leu	
35 40 45	
Asp Asn Asp Ala Ala Ala Val Arg Glu Asp Ala Glu Leu Lys Leu Glu	
50 55 60	
Ile Ala Glu Leu Lys Ser Met Phe Ile Glu Arg Ala Gln Ala Leu Leu	
65 70 75 80	
His Gly Asp Leu His Thr Gly Ser Ile Met Val Thr Pro Asp Ser Thr	
85 90 95	
Gln Val Ile Asp Pro Glu Phe Ala Phe Tyr Gly Pro Met Gly Tyr Asp	
100 105 110	
Ile Gly Ala Phe Leu Gly Asn Leu Ile Leu Ala Tyr Phe Ser Gln Asp	
115 120 125	
Gly His Ala Asp Gln Ala Asn Asp Arg Lys Ala Tyr	
130 135 140	

<210> 67
 <211> 404
 <212> DNA
 <213> Glycine max

sequence listing

<220>

<221> CDS

<222> (3)..(404)

<223> coding for 5-methylthioribose kinase

<400> 67

ta atc ccc gaa cat gtt cct gaa gtg tat cac ttt gac cgt acc atg	47
Ile Pro Glu His Val Pro Glu Val Tyr His Phe Asp Arg Thr Met	
1 5 10 15	
tct ttg atc ggt atg cgt tac ttg gag ccc cca cat ata atc ctc ata	95
Ser Leu Ile Gly Met Arg Tyr Leu Glu Pro Pro His Ile Ile Leu Ile	
20 25 30	
aaa ggg ttg att gct ggg att gag tac cct ttt ttg gct gaa cac atg	143
Lys Gly Leu Ile Ala Gly Ile Glu Tyr Pro Phe Leu Ala Glu His Met	
35 40 45	
gct gat ttc atg gcg aag aca ctc ttc ttc acg tct ctg ctt ttc cgt	191
Ala Asp Phe Met Ala Lys Thr Leu Phe Phe Thr Ser Leu Leu Phe Arg	
50 55 60	
tcc act gct gac cac aaa cgg gac gtt gcc gaa ttt tgt ggg aat gtg	239
Ser Thr Ala Asp His Lys Arg Asp Val Ala Glu Phe Cys Gly Asn Val	
65 70 75	
gag tta tgc agg ctc act gaa cag gtc gtt ttc tct gac cct tat aaa	287
Glu Leu Cys Arg Leu Thr Glu Gln Val Val Phe Ser Asp Pro Tyr Lys	
80 85 90 95	
gtt tct caa tat aat cgt tgg act tcc ccc tat ctt gat cgt gat gct	335
Val Ser Gln Tyr Asn Arg Trp Thr Ser Pro Tyr Leu Asp Arg Asp Ala	
100 105 110	
gag gct gtt cgg gaa gac aat ctg ctg aag ctt gaa gtt gct gag ctg	383
Glu Ala Val Arg Glu Asp Asn Leu Leu Lys Leu Glu Val Ala Glu Leu	
115 120 125	
aaa tcc aag ttc att gag agc	404
Lys Ser Lys Phe Ile Glu Ser	
130	

<210> 68

<211> 134

<212> PRT

<213> Glycine max

<400> 68

Ile Pro Glu His Val Pro Glu Val Tyr His Phe Asp Arg Thr Met Ser
1 5 10 15
Leu Ile Gly Met Arg Tyr Leu Glu Pro Pro His Ile Ile Leu Ile Lys
20 25 30
Gly Leu Ile Ala Gly Ile Glu Tyr Pro Phe Leu Ala Glu His Met Ala
35 40 45
Asp Phe Met Ala Lys Thr Leu Phe Phe Thr Ser Leu Leu Phe Arg Ser
50 55 60
Thr Ala Asp His Lys Arg Asp Val Ala Glu Phe Cys Gly Asn Val Glu
65 70 75 80

sequence listing

Leu Cys Arg Leu Thr Glu Gln Val Val Phe Ser Asp Pro Tyr Lys Val
85 90 95
Ser Gln Tyr Asn Arg Trp Thr Ser Pro Tyr Leu Asp Arg Asp Ala Glu
100 105 110
Ala Val Arg Glu Asp Asn Leu Leu Lys Leu Glu Val Ala Glu Leu Lys
115 120 125
Ser Lys Phe Ile Glu Ser
130

<210> 69
<211> 21
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 69
cgtgaatacg gcgtggagtc g 21

<210> 70
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 70
cggcaggata atcaggttgg 20

<210> 71
<211> 20
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 71
gtcaacgtaa ccaaccctgc 20